

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: 4498	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: 5/24/03	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: 20	Patent Family _____	WWW/Internet _____
Online Time: 35	Other _____	Other (specify) _____

4

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 17:12:46 ; Search time 16.5 Seconds

(without alignments)
60.105 Million cell updates/sec

Title: US-09-932-613-448
Perfect score: 25
Sequence: 1 XDXLTXLXX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues
Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pbp:*
 - 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pbp:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pbp:*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pbp:*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pbp:*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pbp:*
 - 7: /cgn2_6/ptodata/2/pubpaa/PTCTUS_PUBCOMB.pbp:*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pbp:*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pbp:*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pbp:*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pbp:*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pbp:*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pbp:*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	19	76.0	152	9	US-10-153-344-32
2	19	76.0	173	10	US-09-925-301-1254
3	19	76.0	180	9	US-09-813-153-113
4	19	76.0	188	9	US-09-832-877-159
5	19	76.0	193	3	US-09-764-868-760
6	19	76.0	199	9	US-09-764-868-1137
7	19	76.0	219	9	US-09-813-153-190
8	19	76.0	261	10	US-09-741-669-399
9	19	76.0	296	10	US-09-843-164-4
10	19	76.0	332	9	US-09-738-626-6060
11	19	76.0	335	9	US-09-832-877-106
12	19	76.0	385	9	US-10-260-877-106
13	19	76.0	431	9	US-10-043-487-232
14	19	76.0	431	10	US-09-799-777-34
15	19	76.0	451	10	US-09-815-243-5355
16	19	76.0	452	9	US-10-084-205-26
17	19	76.0	452	10	US-09-815-243-12396
18	19	76.0	452	10	US-09-925-637-26
19	19	76.0	452	10	US-09-932-418-2

Sequence 8, Appli
Sequence 20, Appl
Sequence 5, Appl
Sequence 12089, A
Sequence 2, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 6, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 14, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 5908, Ap
Sequence 50, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 6, Appl
Sequence 6, Appl

9 US-10-146-806-3
10 US-09-931-087A-20
10 US-09-931-087A-5
10 US-09-815-242-12089
10 US-09-843-164-2
9 US-09-945-901-42
9 US-10-007-747-42
9 US-10-038-937-42
10 US-09-843-164-6
9 US-10-001-488B-2
9 US-10-259-864-2
9 US-10-259-864-6
9 US-10-259-864-4
9 US-10-259-864-1
9 US-09-945-901-54
9 US-10-007-747-54
9 US-10-038-937-54
10 US-09-815-242-5908
9 US-09-945-901-50
9 US-10-007-747-50
9 US-10-038-937-50
9 US-09-945-901-48
9 US-10-007-747-48
9 US-10-038-937-48
9 US-09-945-901-6
9 US-10-007-747-6

ALIGNMENTS

RESULT 1
US-10-153-344-32
; Sequence 32, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3: AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/292,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (132)..(143)
; OTHER INFORMATION: Xaa is any amino acid
US-10-153-344-32

Query Match 76.0%; Score 19; DB 9; Length 152;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTXL 8
| | | |
DB 105 DLTSL 110

RESULT 2
US-09-925-301-1254
; Sequence 1254, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1254
LENGTH: 173
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-301-1254

Query Match 76.0%; Score 19; DB 10; Length 173;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTSL 8
| | | |
Db 124 DLSLTL 129

RESULT 3
US-09-813-153-113
Sequence 113, Application US/09813153
Publication No. US20030045459A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: P2023
CURRENT APPLICATION NUMBER: US/09/813,153
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US/09/363,044
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,159
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,165
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,164
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,167
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,162
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,161
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,170
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 113
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (180)
OTHER INFORMATION: Xaa equals stop translation
US-09-813-153-113

Query Match 76.0%; Score 19; DB 9; Length 180;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTSL 8
| | | |
Db 124 DLSLTL 129

RESULT 4

US-09-892-877-159
Sequence 159, Application US/09892877
Publication No. US20030077809A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: P2028P1
CURRENT APPLICATION NUMBER: US/09/892,877
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 159
LENGTH: 188
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (188)
OTHER INFORMATION: Xaa equals stop translation
US-09-892-877-159

Query Match 76.0%; Score 19; DB 9; Length 188;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTSL 8
| | | |
Db 92 DLSLTL 97

RESULT 5

US-09-764-868-760
Sequence 760, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 760
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (86)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (161)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (162)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (175)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-760

Query Match 76.0%; Score 19; DB 9; Length 193;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTSL 8
| | | |
Db 99 DLSLTL 104

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RESULT 6
US-09-764-868-1137
; Sequence 1137, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1137
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (92)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (167)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (181)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1137
Query Match          76.0%; Score 19; DB 9; Length 199;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 105 DSLTSL 110

RESULT 7
US-09-813-153-190
; Sequence 190, Application US/09813153
; Publication No. US20030045459A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023
; CURRENT APPLICATION NUMBER: US/09/813,153
; CURRENT FILING DATE: 2001-03-21
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US/09/363,044
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 190

Query Match          76.0%; Score 19; DB 9; Length 199;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 105 DSLTSL 110

RESULT 8
US-09-741-669-399
; Sequence 399, Application US/09741669
; Patent No. US20020022718A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; proliferation of E. coli
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-669-399
Query Match          76.0%; Score 19; DB 10; Length 261;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 159 DSLTTL 164

RESULT 9
US-09-843-164-4
; Sequence 4, Application US/09843164
; Patent No. US20020061556A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. US20020061556A1 Human Membrane Proteins and Polynucleotic
; FILE REFERENCE: 07705.0014-00000
; CURRENT APPLICATION NUMBER: US/09/843,164
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/199,950
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 296
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-843-164-4
Query Match          76.0%; Score 19; DB 10; Length 296;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
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Db 230 DALTTL 285

RESULT 10
US-09-738-626-6060
; Sequence 6060, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NARAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6060
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6060

Query Match 76.0%; Score 19; DB 9; Length 332;
Best Local Similarity 66.7%; Pred. No. 8.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
Db 78 DALTSL 83

RESULT 11
US-09-892-877-216
; Sequence 216, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; FILE REFERENCE: P2028P1
; CURRENT APPLICATION NUMBER: US/09/892,877
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 216
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-877-216

Query Match 76.0%; Score 19; DB 9; Length 335;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
Db 235 DSUTSL 240

RESULT 12

US-10-260-877-106
; Sequence 106, Application US/10260877
; Publication No. US20030021813A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Chevan, Linda E.
; APPLICANT: Hessler, Paul E.
; APPLICANT: Reich, Karl A.
; TITLE OF INVENTION: ESSENTIAL BACTERIA GENES AND GENOME
; TITLE OF INVENTION: SCANNING IN HAEMOPHILUS INFLUENZAE FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: 'ESSENTIAL GENES'
; FILE REFERENCE: 6565 US P1
; CURRENT APPLICATION NUMBER: US/10/260,877
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/649,145
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 385
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-260-877-106

Query Match 76.0%; Score 19; DB 9; Length 385;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
Db 157 DALTAL 162

RESULT 13
US-10-043-487-232
; Sequence 232, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-232

Query Match 76.0%; Score 19; DB 9; Length 431;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
Db 331 DSUTSL 336

RESULT 14
US-09-799-777-34
; Sequence 34, Application US/09799777
; Patent No. US20020091244A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti

Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/002,485
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34 :
US-09-799-777-34

Query Match 76.0%; Score 19; DB 10; Length 431;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 DXTLXL 8
Db 331 DSLTSL 336

RESULT 15
US-09-815-242-5355
Sequence 5355, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5355
LENGTH: 451
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5355
Query Match 76.0%; Score 19; DB 10; Length 451;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 DXTLXL 8
Db 88 DTLTAL 93

Search completed: May 24, 2003, 17:23:36
Job time : 17.5 secs

GenCore version 5.1.4 p5_457a
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OM protein - protein search, using sw model

Run on: May 24, 2003, 17:10:26 ; Search time 19 Seconds
(without alignments)
15.486 Million cell updates/sec

Title: US-09-932-613-448

Perfect score: 25

Sequence: 1 XXDXLTLXX 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	76.0	33	1	US-08-309-512-12
2	19	76.0	87	2	US-08-461-9908-20
3	19	76.0	275	4	US-09-134-001C-3732
4	19	76.0	316	4	US-09-413-814-14
5	19	76.0	449	1	US-08-831-753-1
6	19	76.0	452	4	US-09-144-918-2
7	19	76.0	500	4	US-09-071-035-396
8	19	76.0	532	4	US-09-655-270A-3
9	19	76.0	532	4	US-09-651-941-3
10	19	76.0	532	4	US-09-955-597-3
11	19	76.0	595	4	US-08-264-578-8
12	19	76.0	667	4	US-09-315-127-5
13	19	76.0	667	4	US-09-315-127-6
14	19	76.0	688	4	US-09-367-206-20
15	19	76.0	703	4	US-09-367-206-5
16	19	76.0	771	4	US-09-090-793-8
17	19	76.0	774	2	US-08-231-193A-42
18	19	76.0	774	2	US-08-486-273A-42
19	19	76.0	774	3	US-08-480-474-42
20	19	76.0	774	3	US-08-940-086A-42
21	19	76.0	774	4	US-08-940-035A-42
22	19	76.0	774	4	US-08-935-105A-42
23	19	76.0	774	4	US-08-648-797-42
24	19	76.0	780	1	US-08-375-709-13
25	19	76.0	780	1	US-08-752-929-13
26	19	76.0	795	1	US-07-716-827C-5
27	19	76.0	1012	1	US-08-219-262B-10

28	19	76.0	1012	3	US-09-031-655-10
29	19	76.0	1070	4	US-09-091-042A-2
30	19	76.0	1074	4	US-09-071-035-359
31	19	76.0	1074	4	US-09-071-035-394
32	19	76.0	1214	2	US-08-231-193A-54
33	19	76.0	1214	2	US-08-486-273A-54
34	19	76.0	1214	3	US-08-480-474-54
35	19	76.0	1214	3	US-08-940-066A-54
36	19	76.0	1214	4	US-08-940-035A-54
37	19	76.0	1214	4	US-08-935-105A-54
38	19	76.0	1214	4	US-09-648-797-54
39	19	76.0	1219	2	US-08-231-193A-50
40	19	76.0	1219	2	US-08-486-273A-50
41	19	76.0	1219	3	US-08-480-474-50
42	19	76.0	1219	3	US-08-940-086A-50
43	19	76.0	1219	4	US-08-940-035A-50
44	19	76.0	1219	4	US-08-935-105A-50
45	19	76.0	1219	4	US-09-648-797-50

ALIGNMENTS

RESULT 1
US-08-309-512-12
; Sequence 12, Application US/08309512
; Patent No. 5759828
; GENERAL INFORMATION:
; APPLICANT: Tal, Ronny
; APPLICANT: Ben-Ziman, Moshe
; APPLICANT: Gelfand, David H.
; APPLICANT: Ben-Bassat, Arie
; APPLICANT: Calhoun, Roger D.
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/309,512
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,218
; FILING DATE: 29-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bortner, Scott R.
; REGISTRATION NUMBER: 34,298
; REFERENCE/DOCKET NUMBER: 8145-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Acetobacter xylinum
US-08-309-512-12

Query Match 76.0%; Score 19; DB 1; Length 33;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 DLTXTL 8
 | | | |
 Db 9 DLTTL 14

RESULT 2

US-08-461-990B-20
 ; Sequence 20, Application US/08461990B
 ; Patent No. 5851810
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN S. BLANCHARD
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING RHODOCOCCLUS
 ; TITLE OF INVENTION: PHENYLALANINE DEHYDROGENASE
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
 ; STREET: 90 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10016
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/461,990B
 ; FILING DATE: JUNE 5, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CRAIG J. ARNOLD
 ; REGISTRATION NUMBER: 34,287
 ; REFERENCE/DOCKET NUMBER: 96760/370
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 697-5995
 ; TELEFAX: (212) 266-0854 or 286-0082
 ; TELEX: TWX 710-581-4766
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 87
 ; TYPE: AMINO ACID
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: PROTEIN
 ; DESCRIPTION: NO
 ; HYPOTHEICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: C. SYMBIOSUM
 ; INDIVIDUAL ISOLATE: GLUTAMATE DEHYDROGENASE
 ; US-08-461-990B-20

Query Match 76.0%; Score 19; DB 2; Length 87;
 Best Local Similarity 66.7%; Pred. No. 88;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTXTL 8
 | | | |
 Db 36 DLTTL 41

RESULT 3

US-09-134-001C-3732
 ; Sequence 3732, Application US/09134001C
 ; Patent No. 5380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3732
 ; LENGTH: 275
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-3732

Query Match 76.0%; Score 19; DB 4; Length 275;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTXTL 8
 | | | |
 Db 153 DLTAL 158

RESULT 4

US-09-413-814-14
 ; Sequence 14, Application US/09413814
 ; Patent No. 6225064
 ; GENERAL INFORMATION:
 ; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 ; APPLICANT: Bristol-Myers Squibb, Co.
 ; APPLICANT: Beyer, Stefan
 ; APPLICANT: Bioecker, Helmut
 ; APPLICANT: Brandt, Petra
 ; APPLICANT: Cino, Paul M
 ; APPLICANT: Dougherty, Brian A
 ; APPLICANT: Goldberg, Steven L
 ; APPLICANT: Hofle, Gerhard
 ; APPLICANT: Mueller, Joachim
 ; APPLICANT: Reichenbach, Hans
 ; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 ; TITLE OF INVENTION: heteropolyketide compounds
 ; FILE REFERENCE: PCT/US 99/23535
 ; CURRENT APPLICATION NUMBER: US/09/413,814
 ; CURRENT FILING DATE: 1999-10-07
 ; EARLIER APPLICATION NUMBER: DE 198 46 493.2
 ; EARLIER FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 ; US-09-413-814-14

Query Match 76.0%; Score 19; DB 4; Length 316;
 Best Local Similarity 66.7%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTXTL 8
 | | | |
 Db 212 DLTAL 217

RESULT 5

US-08-831-753-1
 ; Sequence 1, Application US/08831753
 ; Patent No. 5798234
 ; GENERAL INFORMATION:
 ; APPLICANT: ENGEL, PAUL C
 ; APPLICANT: RICE, DAVID
 ; TITLE OF INVENTION: METHOD FOR THE DIRECTED MODIFICATION OF
 ; TITLE OF INVENTION: ENZYMES, MODIFIED ENZYMES AND THEIR USE
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
 STREET: 1100 NEW YORK AVENUE, NW, NINTH FLOOR, EAST
 STREET: TOWER
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/831,753
 APPLICATION NUMBER: US/08/831,753
 FILING DATE: 01-APR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOBBS, ANN S
 REGISTRATION NUMBER: 36830
 REFERENCE/DOCKET NUMBER: 21123/235858
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Clostridium symbiosum
 US-08-831-753-1

Query Match 76.0%; Score 19; DB 1; Length 449;
 Best Local Similarity 66.7%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDLTXL 8
 DB 114 DDLTXL 119

RESULT 6
 US-09-144-918-2
 ; Sequence 2, Application US/09144918
 ; Patent No. 6287807
 ; GENERAL INFORMATION:
 ; APPLICANT: Wallis, Nicola G.
 ; TITLE OF INVENTION: Murf
 ; FILE REFERENCE: GM10098
 ; CURRENT APPLICATION NUMBER: US/09/144,918
 ; EARLIER FILING DATE: 1998-09-01
 ; EARLIER APPLICATION NUMBER: 60/060,682
 ; EARLIER FILING DATE: 1997-09-25
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 452
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-144-918-2

Query Match 76.0%; Score 19; DB 4; Length 452;
 Best Local Similarity 66.7%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDLTXL 8
 DB 88 DDLTXL 93

RESULT 7
 US-09-071-035-396
 ; Sequence 396, Application US/09071035
 ; Patent No. 6448043
 ; GENERAL INFORMATION:
 ; APPLICANT: Gil H. Choi
 ; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 ; NUMBER OF SEQUENCES: 496
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: Maryland
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 ; COMPUTER: HP Vectra 486/33
 ; OPERATING SYSTEM: MSDOS version 6.2
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,035
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: A. Anders Brooks
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PB369P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 396:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 500 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-071-035-396

Query Match 76.0%; Score 19; DB 4; Length 500;
 Best Local Similarity 66.7%; Pred. No. 6.3e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDLTXL 8
 DB 210 DDLTXL 215

RESULT 8
 US-09-655-270A-3
 ; Sequence 3, Application US/09655270A
 ; Patent No. 6329151
 ; GENERAL INFORMATION:
 ; APPLICANT: Rouviere, Pierre B.
 ; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic
 ; FILE REFERENCE: BC1011 US NA
 ; CURRENT APPLICATION NUMBER: US/09/655,270A
 ; CURRENT FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/120,702
 ; PRIOR FILING DATE: 1999-February-19
 ; PRIOR APPLICATION NUMBER: 60/152,542
 ; PRIOR FILING DATE: 1999-September-03
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 3
 ; LENGTH: 532
 ; TYPE: PRT
 ; ORGANISM: Rhodococcus erythropolis HL PM-1
 US-09-655-270A-3

Query Match 76.0%; Score 19; DB 4; Length 532;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DLTSL 8
Db 72 DLTSL 77

RESULT 9

US-09-651-941-3
; Sequence 3, Application US/09651941
; Patent No. 6355470
; GENERAL INFORMATION:
; APPLICANT: ROUVIER, PIERRE E
; APPLICANT: WALTERS, DANA M
; APPLICANT: RAINIER, RUSS
; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
; FILE REFERENCE: BC1022 US NA
; CURRENT APPLICATION NUMBER: US/09/651,941
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,545
; PRIOR FILING DATE: 1999-10-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-651-941-3

Query Match 76.0%; Score 19; DB 4; Length 532;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DLTSL 8
Db 72 DLTSL 77

RESULT 10

US-09-955-597-3
; Sequence 3, Application US/09955597
; Patent No. 6461856
; GENERAL INFORMATION:
; APPLICANT: ROUVIER, PIERRE E
; APPLICANT: WALTERS, DANA M
; APPLICANT: RAINIER, RUSS
; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
; FILE REFERENCE: BC1022 US NA
; CURRENT APPLICATION NUMBER: US/09/955,597
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/152,545
; PRIOR FILING DATE: 1999-10-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-955-597-3

Query Match 76.0%; Score 19; DB 4; Length 532;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DLTSL 8
Db 72 DLTSL 77

RESULT 11

US-08-264-578-8
; Sequence 8, Application US/08264578
; Patent No. 6391566
; GENERAL INFORMATION:
; APPLICANT: FOLDES, Robert L.
; APPLICANT: ADAMS, Sally-Lin
; APPLICANT: KAMBOJ, Rajender
; APPLICANT: DUNCAN, H. Scott
; TITLE OF INVENTION: Modulatory Proteins of Human CNS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,578
; FILING DATE: 23-JUN-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/987,953
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/261/ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-264-578-8

Query Match 76.0%; Score 19; DB 4; Length 595;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DLTSL 8
Db 384 DLTSL 389

RESULT 12

US-09-315-127-5
; Sequence 5, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-315-127-5

Query Match 76.0%; Score 19; DB 4; Length 667;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 DXLTXL 8
Db 549 DSLTSL 554

RESULT 13
US-09-315-127-6
; Sequence 6, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; FILE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315.127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQ ID NO. 4,
; OTHER INFORMATION: envelope protein produced by retroviral vector of
; OTHER INFORMATION: seq. id no. 3
US-09-315-127-6

Query Match 76.0%; Score 19; DB 4; Length 667;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 DXLTXL 8
Db 549 DSLTSL 554

RESULT 14
US-09-367-206-20
; Sequence 20, Application US/09367206
; Patent No. 6326482
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: NSP Molecules
; FILE REFERENCE: P1223R1F
; CURRENT APPLICATION NUMBER: US/09/367,206
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/08847
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/082,767
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 60/113,296
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 20
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-367-206-20

Query Match 76.0%; Score 19; DB 4; Length 688;
Best Local Similarity 66.7%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 DXLTXL 8
Db 72 DSLTSL 77

RESULT 15
US-09-367-206-5
; Sequence 5, Application US/09367206
; Patent No. 6326482
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: NSP Molecules
; FILE REFERENCE: P1223R1F
; CURRENT APPLICATION NUMBER: US/09/367,206
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/08847
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/082,767
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 60/113,296
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 5
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-367-206-5

Query Match 76.0%; Score 19; DB 4; Length 703;
Best Local Similarity 66.7%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 DXLTXL 8
Db 87 DSLTSL 92

Search completed: May 24, 2003, 17:13:59
Job time : 20 secs

OM protein - protein search, using sw model

Run on: May 24, 2003, 17:08:56 ; Search time 14 Seconds
(without alignments)
68.667 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKLWL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	71.9	870	1 GNMVJA	pol polyprotein -
2	45	70.3	383	2 B84608	hypothetical prote
3	45	70.3	482	2 G83928	hypothetical prote
4	43	67.2	567	2 AC0754	probable membrane
5	43	67.2	570	2 T20166	hypothetical prote
6	43	67.2	388	1 GNLJHD	pol polyprotein -
7	42	65.6	293	2 T05419	hypothetical prote
8	42	65.6	374	2 B85421	probable polygalac
9	42	65.6	374	2 T04672	polysialacturonase
10	42	65.6	392	2 T09371	hypothetical prote
11	41	64.1	655	2 F82138	G3DEF family prote
12	41	64.1	672	2 H83135	hypothetical prote
13	40	62.5	202	2 S16442	MIPP protein - mou
14	40	62.5	345	2 A43586	hypothetical prote
15	40	62.5	378	2 T47407	hypothetical prote
16	40	62.5	519	2 B87353	hypothetical prote
17	39	60.9	157	2 S49622	crtk protein - Rho
18	39	60.9	158	2 A57438	tryptophan-rich se
19	39	60.9	176	1 F64725	probable NAD(P)H2
20	39	60.9	176	2 A85486	probable NAD(P)H o
21	39	60.9	176	2 A90635	probable NAD(P)H o
22	39	60.9	176	2 A10512	probable NAD(P)H o
23	39	60.9	308	1 WMLJ51	bel-1 protein - si
24	39	60.9	311	2 S18740	bel-1 protein - sim
25	39	60.9	333	2 S42424	hypothetical prote
26	39	60.9	335	2 T48319	hypothetical prote
27	39	60.9	365	2 T08577	hypothetical prote
28	39	60.9	430	2 T20170	hypothetical prote
29	39	60.9	480	2 T20168	hypothetical prote

30	39	60.9	551	2 D71969	L-lactate permease
31	39	60.9	551	2 B64537	L-lactate permease
32	39	60.9	983	2 B86989	probable integral
33	39	60.9	2183	2 T37218	hypothetical prote
34	38	59.4	190	2 B83990	hypothetical prote
35	38	59.4	206	2 G69057	hypothetical prote
36	38	59.4	295	2 T32202	hypothetical prote
37	38	59.4	321	2 T50966	hypothetical prote
38	38	59.4	341	2 B83298	conserved hypothet
39	38	59.4	361	2 A13513	Airase virB11 homo
40	38	59.4	380	2 T00683	hypothetical prote
41	38	59.4	491	2 AC2650	glucose-6-phosphat
42	38	59.4	503	2 B97432	glucose-6-phosphat
43	38	59.4	549	2 C71969	L-lactate permease
44	38	59.4	549	2 D64537	L-lactate permease
45	38	59.4	560	2 F81423	L-lactate permease

ALIGNMENTS

RESULT 1

GNMVJA

pol polyprotein - sheep pulmonary adenomatosis virus

N;Contains: endonuclease (EC 3.1.1.-); RNA-directed DNA polymerase (EC 2.7.7.49)

C;Species: sheep pulmonary adenomatosis virus

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Apr-1994

C;Accession: C42740

R;York, D.F.; Vigne, R.; Verwoerd, D.W.; Querat, G.

J. Virol. 66, 4930-4939, 1992

A;Title: Nucleotide sequence of the jaagsiekte retrovirus, an exogenous and endogenous

A;Reference number: A42740; MUID:92333675; PMID:1629959

A;Accession: C42740

A;Molecule type: Genomic RNA

A;Residues: 1-870 <YOR>

A;Cross-references: GB:M80216

C;Comment: This protein is likely to be expressed as a gag-pol polyprotein.

C;Comment: The precise boundary between RNA-directed DNA polymerase and endonuclease

C;Genetics:

A;Gene: pol

A;Start codon: UCA

C;Superfamily: pol polyprotein

C;Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse tra

Query Match 71.9%; Score 46; DB 1; Length 870;

Best Local Similarity 77.8%; Pred. No. 6.6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9

Db 813 WKDPLTNLW 821

RESULT 2

B84608

hypothetical protein At2g22030 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C;Accession: B84608

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosomes 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84608

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-383 <STO>

A;Cross-references: GB:AE002093; NID:94587593; PIDN:RAD25821.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g22030

A;Map position: 2

C;Superfamily: caffeoyl-CoA 3-O-methyltransferase

Query Match 70.3%; Score 45; DB 2; Length 383;
Best Local Similarity 65.7%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||||
DB 288 WYDPKQKW 296

RESULT 3

G83928
hypothetical protein BH2231 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: G83928
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-482 <STO>
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BA05950.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2231

Query Match 70.3%; Score 45; DB 2; Length 482;
Best Local Similarity 77.8%; Pred. No. 5.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||||
DB 443 WYRPLTWLW 451

RESULT 4

AC0754
probable membrane protein STY2194 [imported] - Salmonella enterica subsp. enterica serov
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AC0754
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AC0754
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-567 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05734.1; PID:g16503227; GSPDB:GN00176
C;Genetics:
A;Gene: STY2194

Query Match 67.2%; Score 43; DB 2; Length 567;
Best Local Similarity 56.7%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||||
DB 396 WHDPLTRLY 404

RESULT 5

T20166
hypothetical protein C53A5.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20166
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19232
A;Accession: T20166
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-570 <WIL>
A;Cross-references: EMBL:Z81486; PIDN:CA03987.1; GSPDB:GN000023; CESP:C53A5.6
A;Experimental source: clone C53A5
C;Genetics:
A;Gene: CESP:C53A5.6
A;Map position: 5
A;Introns: 17/1; 86/3; 290/1; 360/3; 428/1

Query Match 67.2%; Score 43; DB 2; Length 570;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9
|||||
DB 492 YDPLTKSW 499

RESULT 6

GNLJHD
pol polyprotein - squirrel monkey retrovirus SMRV-H (SMRV-HLB)
N;Contains: endonuclease (EC 3.1.-.-); RNA-directed DNA polymerase (EC 2.7.7.49)
C;Species: squirrel monkey retrovirus SMRV-H
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 01-May-1998
C;Accession: C31827
R;Oda, T.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Akiyama, K.; Mitsunobu, F.
Virology 167, 468-476, 1988
A;Title: Molecular cloning, complete nucleotide sequence, and gene structure of the f
A;Reference number: A31827; MUID:89073750; PMID:3201749
A;Accession: C31827
A;Molecule type: DNA
A;Residues: 1-888 <ODA>
A;Comment: The pol polyprotein contains reverse transcriptase and endonuclease; howev
C;Genetics:
A;Gene: pol
C;Superfamily: pol polyprotein
C;Keywords: endonuclease; hydrolase; nucleotidyltransferase; polypeptide; reverse tra

Query Match 67.2%; Score 43; DB 1; Length 888;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
|||||
DB 821 WRDPLTSW 829

RESULT 7

T05419
hypothetical protein F28A23.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jan-2000
C;Accession: T05419
R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.
submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15415
A;Accession: T05419
A;Molecule type: DNA
A;Residues: 1-293 <BEV>
A;Cross-references: EMBL:AL021961
A;Experimental source: cultivar Columbia; BAC clone F28A23
C;Genetics:
A;Map position: 4
A;Introns: 66/3
A;Note: F28A23.70

C;Superfamily: caffeoyl-CoA 3-O-methyltransferase

Query Match 65.6%; Score 42; DB 2; Length 293;
Best Local Similarity 55.6%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9

|||||:|

Db 244 WYDKERWV 252

RESULT 8

B85421

C;Species: Arabidopsis thaliana [mouse-ear cress]

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001

C;Accession: B85421

R;Anonymous: The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: B85421

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-374 <STO>

A;Cross-references: GB:NC_001268; NID:g7270518; PIDN:CAB80283.1; GSPDB:EN00140

C;Genetics:

A;Gene: At4g35670

A;Map position: 4

C;Superfamily: polygalacturonase

Query Match 65.6%; Score 42; DB 2; Length 374;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 10

|||||:

Db 91 WSDPISRWWI 100

RESULT 9

T04672

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Nov-2000

C;Accession: T04672

R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes,

submitted to the Protein Sequence Database, July 1998

A;Reference number: Z15381

A;Accession: T04672

A;Molecule type: DNA

A;Residues: 1-374 <BEV>

A;Cross-references: EMBL:AL031135

A;Experimental source: cultivar Columbia; BAC clone F8D20

C;Genetics:

A;Map position: 4

A;Note: intron positions not resolved

A;Note: F8D20.180

C;Superfamily: polygalacturonase

Query Match 65.6%; Score 42; DB 2; Length 374;

Best Local Similarity 40.0%; Pred. No. 13;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 10

|||||:

Db 91 WSDPISRWWI 100

RESULT 10

T09371

C;Species: Arabidopsis thaliana (mouse-ear cress)

hypothetical protein F23K16.180 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999

C;Accession: T09371

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.I.

submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16652

A;Accession: T09371

A;Molecule type: DNA

A;Residues: 1-392 <BEV>

A;Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.180

A;Experimental source: cultivar Columbia; BAC clone F23K16

C;Genetics:

A;Gene: AtSP:F23K16.180

A;Map position: 4

C;Superfamily: caffeoyl-CoA 3-O-methyltransferase

Query Match 65.6%; Score 42; DB 2; Length 392;

Best Local Similarity 55.6%; Pred. No. 14;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9

|||||:

Db 297 WYDTMARLW 305

RESULT 11

F82138

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: F82138

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 405, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: F82138

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-655 <HEI>

A;Cross-references: GB:AE004269; GB:AE003952; NID:g9656466; PIDN:AAF95082.1; GSPDB:GNC

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC1934

A;Map position: 1

Query Match 64.1%; Score 41; DB 2; Length 655;

Best Local Similarity 75.0%; Pred. No. 36;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 8

|||||:

Db 213 WYDPLTKLW 220

RESULT 12

H83315

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C;Accession: H83315

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li

lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: H83315

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-672 <STO>

A;Cross-references: GB:AE004692; GB:AE004091; NID:g9949701; PIDN:AG05023.1; GSPDB:GNC

A;Experimental source: strain PA01

C;Genetics:
A;Gene: PA2635
C;Superfamily: Campylobacter jejuni hypothetical protein Cj0145

Query Match 64.1%; Score 41; DB 2; Length 672;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
|:|:|:|:
Db 566 WFDPEGLW 575

RESULT 13

S16442

MIPP protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C;Accession: S16442; S16443; S19092

R;Chang-Yeh, A.; Mold, D.E.; Huang, R.C.C.

Nucleic Acids Res. 19, 3667-3672, 1991

A;Title: Identification of a novel murine IAP-promoted placenta-expressed gene.

A;Reference number: S16442; MUID:91305114; PMID:1906605

A;Accession: S16442

A;Molecule type: mRNA

A;Residues: 1-202 <CHA>

A;Cross-references: EMBL:X58523; NID:G52733; PIDN:CAA41413.1; PID:G52734

A;Note: the authors translated the codon GCT for residue 20 as Gln, TCA for residue 21 a

A;Accession: S16443

A;Molecule type: DNA

A;Residues: 1-41 <CHAL>

A;Cross-references: EMBL:X58524

R;Chang-Yeh, A.

submitted to the EMBL Data Library, March 1991

A;Reference number: S19092

A;Accession: S19092

A;Molecule type: DNA

A;Residues: 1-25, 'AVDWEVVCATGOSMLW' <CHAZ>

A;Cross-references: EMBL:X58524; NID:G52731; PIDN:CAA41414.1; PID:G52732

A;Note: the difference at the carboxyl end is due to a frameshift error

Query Match 62.5%; Score 40; DB 2; Length 202;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9

|:|:|:|:

Db 9 YDVTQW 16

RESULT 14

A43586

hypothetical protein 1 - Salmonella dublin plasmid pSDL2

C;Species: Salmonella dublin

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999

C;Accession: A43586

R;Krause, M.; Harwood, J.; Fierer, J.; Guiney, D.

Infect. Immun. 59, 1860-1863, 1991

A;Title: Genetic analysis of homology between the virulence plasmids of Salmonella dublin

A;Reference number: A43586; MUID:91209947; PMID:1840573

A;Accession: A43586

A;Molecule type: DNA

A;Residues: 1-345 <KRA>

A;Cross-references: GB:M58505; NID:G154215; PIDN:AAA27173.1; PID:G154216

C;Genetics:

A;Genome: plasmid

Query Match 62.5%; Score 40; DB 2; Length 345;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10

|:|:|:|:

Db 292 WLNPIERLWL 301

RESULT 15

T47407

hypothetical protein F23N14.90 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress);

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000

C;Accession: T47407

R;Bloeker, H.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quettier, F.; Salano

submitted to the Protein Sequence Database, March 2000

A;Reference number: 224465

A;Accession: T47407

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-378 <BLO>

A;Cross-references: EMBL:AL138638

A;Experimental source: cultivar Columbia; BAC clone F23N14

C;Genetics:

A;Map position: 3

A;Note: F23N14.90

C;Superfamily: caffeoyl-CoA 3-O-methyltransferase

Query Match

Best Local Similarity 62.5%; Score 40; DB 2; Length 378;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9

|:|:|:|:

Db 280 WYDSEKLM 288

Search completed: May 24, 2003, 17:13:17

Job time: 16 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 17:01:16 ; Search time 7 Seconds
(without alignments)
59.252 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKLWL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	71.9	870	1	POL JSRV
2	43	67.2	567	1	YEDQ_SALTI
3	43	67.2	570	1	YEDQ_SALTY
4	43	67.2	888	1	POL_SMRVH
5	40	62.5	584	1	IPP_HUMAN
6	40	62.5	584	1	IPP_MOUSE
7	39	60.9	176	1	YABF_ECOLI
8	39	60.9	308	1	BEL1_SFVL
9	39	60.9	333	1	YASD_MYCSM
10	39	60.9	491	1	GAPD_RHIME
11	39	60.9	983	1	V644_MYCLE
12	38	59.4	538	1	C1WA_HUMAN
13	38	59.4	538	1	C1WA_RAT
14	38	59.4	1195	1	METH_SYNY3
15	38	59.4	1576	1	Y1K3_CABEL
16	37.5	58.6	301	1	DAPA_CORGL
17	37	57.8	315	1	Y1123_CABEL
18	37	57.8	363	1	YK32_YEAST
19	37	57.8	382	1	ERG6_YEAST
20	37	57.8	384	1	YB64_SCHPO
21	37	57.8	388	1	CARA_ANASO
22	37	57.8	681	1	RP3A_MOUSE
23	37	57.8	684	1	RP3A_RAT
24	37	57.8	694	1	RP3A_HUMAN
25	37	57.8	704	1	RP3A_BOVIN
26	37	57.8	872	1	SCD1_SCHPO
27	37	57.8	985	1	DPOL_HSV1
28	37	57.8	1105	1	Y3GE_ECOLI
29	37	57.8	1337	1	DEXT_STRDO
30	36.5	57.0	1206	1	METH_MYCLE
31	36	56.2	317	1	Y302_MYCOE
32	36	56.2	399	1	O42B_DROME
33	36	56.2	427	1	Y6271_ESCHERICHIA

34 36 56.2 469 1 AR11 MOUSE
35 36 56.2 503 1 AR11 DROME
36 36 56.2 557 1 AR11 HUMAN
37 36 56.2 700 1 CHAC_PEDHE
38 36 56.2 850 1 DEXT_STRMO
39 36 56.2 863 1 POL_IPHA
40 36 56.2 1276 1 PHY2_SYNY3
41 36 56.2 1369 1 MOKE_SCHPO
42 35 54.7 115 1 YF70_METJA
43 35 54.7 299 1 RNHL_HUMAN
44 35 54.7 301 1 RNHL_MOUSE
45 35 54.7 315 1 YPQR_ACICA

ALIGNMENTS

RESULT 1

POL JSRV STANDARD; PRT; 870 AA.
AC P31623;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P05 polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);
DE Endonuclease].
GN POL.
OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)
OC Viruses; Retroviral viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11746;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333675; PubMed=1629959;
RA York D.F., Vigne R., Verwoerd D.W., Querat G.;
RT "Nucleotide sequence of the Jaagsiekte retrovirus, an exogenous and
endogenous type D and B retrovirus of sheep and goats.";
RL J. Virol. 66:4930-4939(1992).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(n).
CC -!- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -!- MISCELLANEOUS: THIS PROTEIN IS PROBABLY EXPRESSED AS A FUSED
GAG-PRO-POL POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING.
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CC -----
CC EMBL; M80216; AAA89182.1; ALT_INIT.
DR PIR; C42740; GNMVJA.
DR HSSP; P03355; LMML.
DR InterPro; IPR001037; Integrase C.
DR InterPro; IPR003308; Integrase_Zn.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR001584; Rve.
DR Pfam; PF00075; rntse; 1.
DR Pfam; PF00078; rvt; 1.
DR Pfam; PF00552; rntse; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF02022; Integrase_Zn; 1.
KW Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
KW Endonuclease; Polyprotein.
SQ SEQUENCE 870 AA; 99312 MW; CFADEAF8D879C033 CRC64;

Query Match 71.9%; Score 46; DB 1; Length 870;
Best Local Similarity 77.8%; Pred. NO. 2.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 WYDPLTKLM 9
DB 813 WKDPLTKLM 821

RESULT 2
ID YEDQ_SALTY STANDARD; PRT; 567 AA.
AC Q825R0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Hypothetical protein yedQ.
GN YEDQ OR STY2194.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=601;
RN [1]

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EMBL; A5008788; AAL20897.1; -
StyGene; SG23222; yedQ.
InterPro; IPR000160; GDEF.
Pfam; PF00990; GDEF; 1.
SMART; SM00267; DUF1; 1.
TIGRFAMs; TIGR00254; GDEF; 1.
Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT SEQUENCE 360 380 POTENTIAL.
SQ SEQUENCE 570 AA; 65429 MW; BF8DF0CF949925 CRC64;

Query Match 67.2%; Score 43; DB 1; Length 567;
Best Local Similarity 66.7%; Pred. No. 6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLM 9
DB 399 WHDPLTKLM 407

RESULT 4
ID POL_SMRVH STANDARD; PRT; 888 AA.
AC P03364;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE POL polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);
Endonuclease].
GN POL.
OS Squirrel monkey retrovirus (SMRV-H) (SMRV-HLB).
OC Viruses; Retroviral viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11856;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89073750; PubMed=3201749;
RA Oda T., Ikeda S., Watanabe S., Hattushika M., Akiyama K.,
RA Mitsunobu F.,
RT "Molecular cloning, complete nucleotide sequence, and gene structure
of the provirus genome of a retrovirus produced in a human
lymphoblastoid cell line."
RL Virology 167:468-476(1988).
RN [2]
RP SEQUENCE OF 595-774 FROM N.A.
RX MEDLINE=84097535; PubMed=6197754;
```


DR PIR: S16442; S16442.
DR PIR: S16443; S16443.
DR PIR: S19092; S19092.
DR MGD: MGI:96581; Ipp.
DR InterPro: IPR000210; BTB POZ.
DR InterPro: IPR001738; Kelch.
DR Pfam: PF00451; BTB; 1.
DR Pfam: PF01344; Kelch; 6.
DR PRINTS: PR00501; KELCHREPEAT.
DR SMART: SM00225; BTB; 1.
DR PROSITE: PS00097; BTB; 1.
KW Cytoskeleton; Actin-binding; Repeat.
FT DOMAIN 37 104
FT REPEAT 296 343
FT REPEAT 344 390
FT REPEAT 391 437
FT REPEAT 439 485
FT REPEAT 487 533
FT REPEAT 535 583
FT REPEAT 584 634
FT CONFLICT 553 556 LDSV -> FGLS (IN REF. 2).
SQ SEQUENCE 584 AA; 65342 MW; 7D108AB6F5FA8B75 CRC64;
Query Match 62.5%; Score 40; DB 1; Length 584;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 YDPLTKLW 9
DB 363 YDFVTKQW 370
RESULT 7
YABF_ECOLI STANDARD; PRT; 176 AA.
ID YABF_ECOLI
AC P31577; P75629; PRT; 176 AA.
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative NAD(P)H oxidoreductase yabF (EC 1.6.99.-).
GN YABF OR B0046.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=K12;
RA MEDLINE=923334977; PubMed=1630901;
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RA "Systematic sequencing of the Escherichia coli genome: analysis of
RA the 0-2.4 min region";
RA Nucleic Acids Res. 20:3305-3308(1992).
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=K12 / MGI1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12";
RA Science 277:1233-1238(1997).
CC -!- SIMILARITY: BELONGS TO THE NAD(P)H DEHYDROGENASE (QUINONE) FAMILY.
CC
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CC
CC EMBL: X54482; -; NOT ANNOTATED_CDS.
CC EMBL: M74039; AAA47802.1; -.
DR PIR: B39924; WMLJSL.
DR PIR: S18740; S18740.
DR InterPro: IPR004956; Foamy BEL.
DR Pfam: PF03274; Foamy BEL; 1.
KW Transcription regulation; Activator.
FT CONFLICT 89 89 D -> N (IN REF. 2).
FT CONFLICT 119 119 D -> N (IN REF. 2).
FT CONFLICT 257 257 S -> G (IN REF. 2).
SQ SEQUENCE 308 AA; 35311 MW; 7E280B0EPEB21D992 CRC64;
Query Match 50.9%; Score 39; DB 1; Length 308;
Best Local Similarity 56.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 YDPLTKLW 10

Qy 2 YDPLTKLWL 10

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Db 155 YDPETELMW 163
|||||:
YASD MYCSM
ID YASD MYCSM STANDARD; PRT; 333 AA.
AC P41402;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 35.9 kDa protein in ASD 3' region (ORF).
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 607 / mc(2)16 / NRRL B-692;
RA MEDLINE=94254720; PubMed=7910936;
RA Cirillo J.D., Weisbrod T.R., Pascopella L., Bloom B.R.,
RA Jacobs W.R. Jr.;
RT "Isolation and characterization of the aspartokinase and aspartate
RT semialdehyde dehydrogenase operon from mycobacteria.";
RL Mol. Microbiol. 11:629-639 (1994).
CC -----
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CC -----
DR EMBL; AF045609; AAD12043.1;
DR EMBL; AL591784; CAC45276.1;
DR HSP; P11411; IDPG
DR InterPro; IPR001282; G6PD.
DR Pfam; PF00479; G6PD; 1.
DR Pfam; PF02781; G6PD; 1.
DR ProDom; PD001129; G6PD; 1.
DR TIGRFAMs; TIGR00871; zwf; 1.
DR PROSITE; PS00069; G6P DEHYDROGENASE; 1.
KW Oxidoreductase; NADP; Glucose metabolism; Complete proteome.
FT ACT_SITE 184 184 BY SIMILARITY.
FT CONFLICT 401 401 R -> T (IN REF. 1).
SQ SEQUENCE 491 AA; 55301 MW; 0D8B1AFD094E1775 CRC64;

Query Match 60.9%; Score 39; DB 1; Length 491;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WYDPLTKLW 9
| | | | |
Db 448 WIDPILKAW 456

RESULT 11
Y644 MYCLE STANDARD; PRT; 983 AA.
AC Q9CCM6; C32904;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein ML0644.
GN ML0644 OR MLCB1779.46.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=IN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011 (2001).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC CC -!- SIMILARITY: BELONGS TO THE UPF0182 FAMILY.
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CC CC
CC DR EMBL; AL583919; CAC30153.1; -.
CC DR EMBL; Z95271; CAB11027.1; ALT_INIT.
CC DR Leproma; ML0644; -.
CC DR InterPro; IPR005372; UPF0182.
CC DR Pfam; PF03699; UPF0182; 1.
CC KW Hypothetical protein; Transmembrane; Complete proteome.
CC FT TRANSMEM 20 37 POTENTIAL.
CC FT TRANSMEM 63 85 POTENTIAL.
CC FT TRANSMEM 113 135 POTENTIAL.
CC FT TRANSMEM 169 191 POTENTIAL.
CC FT TRANSMEM 212 229 POTENTIAL.
CC FT TRANSMEM 260 277 POTENTIAL.
CC FT TRANSMEM 284 306 POTENTIAL.
CC SQ SEQUENCE 983 AA; 107556 MW; BC8AA30433CA594F CRC64;

Query Match 60.8%; Score 39; DB 1; Length 983;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLWL 10
    ||| |.
DB 666 YDPLVKWVM 674

RESULT 12
CIWA HUMAN
ID CIWA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q9HB59;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium
DE channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KCNK10 OR TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20435789; PubMed=10890510;
RA Lesage P., Terrenoire C., Romey G., Lazdunski M.;
RT "Human TREK2, a 2p domain mechano-sensitive K+ channel with multiple
RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,
RT G1, and Gq protein-coupled receptors.";
RL J. Biol. Chem. 275:28398-28405(2000).
CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
CC UNSATURATED FREE FATTY ACIDS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PANCREAS AND KIDNEY
CC AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE.
CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC
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CC CC EMBL; AF279890; AAG15191.1; -.
CC CC Genew; HGNC:6273; KCNK10.
CC DR InterPro; IPR003280; K+channel_2pore.
CC DR InterPro; IPR001622; K+channel_pore.
CC DR InterPro; IPR000636; M+channel_nlg.
CC DR Pfam; PF00520; Ion_trans; 1.
CC DR PRINTS; PR01333; 2FORECHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
CC Glycoprotein.
CC FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 72 92 POTENTIAL.
CC FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).
CC FT TRANSMEM 182 202 POTENTIAL.
CC FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 234 254 POTENTIAL.
CC FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).
CC FT TRANSMEM 299 319 POTENTIAL.
CC FT DOMAIN 320 338 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;

Query Match 59.4%; Score 38; DB 1; Length 538;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
    ||| |.
DB 295 WYKPLVWFMI 304

RESULT 13
CIWA RAT
ID CIWA_RAT STANDARD; PRT; 538 AA.
AC Q9JTS4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium
DE channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KCNK10 OR TREK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20298807; PubMed=10747911;
RA Bang H., Kim Y., Kim D.;
RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
RT family.";
RL J. Biol. Chem. 275:17412-17419(2000).
CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
CC UNSATURATED FREE FATTY ACIDS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN,
CC AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC
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DR EMBL; AF196965; AAF75132.1;
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR000636; M-channel_nig.
DR InterPro; IPR003976; Trek_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01333; 2FORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
DR Ionic_channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).
FT TRANSSEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 299 319 POTENTIAL.
FT DOMAIN 320 538 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 538 AA; 59800 MW; 1FF33F0A52B97B4 CRC64;

Query Match 59.4%; Score 38; DB 1; Length 538;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YDPLTKLWL 10
Db 295 WKPLVWFNI 304

RESULT 14
METH SYN3
ID METH SYN3 STANDARD; PRT; 1195 AA.
AC Q55786;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 5-methyltetrahydrofolate-homocysteine methyltransferase (EC 2.1.1.13)
DE (Methionine synthase, vitamin-B12 dependent isozyme) (MS).
DE METH OR SLR0212.
GN Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + L-homocysteine =
CC tetrahydrofolate + L-methionine.
CC -1- COPACTOR: COBALAMIN (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE DE NOVO BIOSYNTHESIS OF METHIONINE.
CC -1- SIMILARITY: BELONGS TO THE VITAMIN-B12 DEPENDENT METHIONINE
CC SYNTHASE FAMILY.
CC
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CC
CC EMBL; D64002; BAB10438.1;
CC HSRF; F13009; IEMI.
DR InterPro; IPR003312; B12-binding.
DR InterPro; IPR003759; CoMet_synt_B12.

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DR InterPro; IPR000489; Dhdropt_synt.
DR InterPro; IPR004223; Met_synt_B12.
DR InterPro; IPR003726; S_methyl_trans.
DR Pfam; PF00809; Pterin_bind; 1.
DR Pfam; PF02310; B12-binding; 1.
DR Pfam; PF02574; S-methyl_trans; 1.
DR Pfam; PF02607; B12-binding_2; 1.
DR Pfam; PF02965; Met_synt_B12; 1.
KW transferase; Methyltransferase; Methionine biosynthesis; Vitamin B12;
FT DOMAIN 735 812 COBALAMIN-BINDING (POTENTIAL).
FT METAL 737 737 COBALT (POTENTIAL).
SQ SEQUENCE 1195 AA; 132539 MW; 1D9635B1B1DB583 CRC64;

Query Match 59.4%; Score 38; DB 1; Length 1195;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YDPLTKL 8
Db 611 YDPLTKL 617

RESULT 15
YLK3 CAEL
ID YLK3 CAEL STANDARD; PRT; 1576 AA.
AC P41951; Q950P7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative serine/threonine-protein kinase D1044.3 in chromosome III
DE (EC 2.7.1.1).
GN D1044.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Waterston R.;
RA Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RN REVISIONS, AND ALTERNATIVE SPLICING.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b; are
CC produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STRONG, TO ZC84.1.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U00065; AAK68286.1;
CC EMBL; U00065; AAL27237.1;
CC HSP; Q63450; 1A06.
CC WormPep; D1044.3a; CE27894.
CC WormPep; D1044.3b; CE29743.
DR InterPro; IPR000719; Suk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR002899; WRI1/EB.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01683; EB; 12.
DR PRODOM; PD000001; Suk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00289; WRI; 12.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS0011; PROTEIN KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding; Alternative splicing.
FT DOMAIN 431 703 PROTEIN KINASE.
FT NE_BIND 437 445 ATP (BY SIMILARITY).
FT BINDING 461 461 ATP (BY SIMILARITY).
FT ACT_SITE 569 569 BY SIMILARITY.
FT VARSPLIC 1 904 MISSING (IN ISOFORM B).
FT VARSPLIC 905 1012 MISSING (IN ISOFORM B).
FT ACT_SITE 569 569 SPEIQMNLGFSDFRPVLVQSHINGYKQKQVTKITYEQLS
FT VARSPLIC 905 1012 ACIECLIAENPAKGVPHRTRAVVILRRDLLVLGQVVMILV
FT VARSPLIC 905 1012 PTITVYVIRQIRHVSLLAAILVYTEYE -> MEETCSSEPKK
FT VARSPLIC 905 1012 SNIISFTIMWKLLKRVPPIMICLFFELLLOIFVLSVVSQCPP
FT VARSPLIC 905 1012 GLPLFNSNPNQPLTCTPDQACSCYSSSSGSRFGICQYA
FT VARSPLIC 905 1012 STYNNYICCYSTNTQ (IN ISOFORM B).
SQ SEQUENCE 1576 AA; 174677 MW; 3A11B573E813498 CRC64;
Query Match 59.4%; Score 38; DB 1; Length 1576;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 YDPLTKLW 9
Db 659 YDPLNEMW 666

Search completed: May 24, 2003, 17:11:44
Job time : 9 secs

OM protein - protein search, using sw model

Run on: May 24, 2003, 17:06:21 ; Search time 25 Seconds
(without alignments)
82,419 Million cell updates/sec

Title: US-09-932-613-457
Perfect score: 64
Sequence: 1 WYDPLTKLWL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.*

- 1: sp archaea.*
- 2: sp bacteria.*
- 3: sp fungi.*
- 4: sp human.*
- 5: sp invertebrate.*
- 6: sp mammal.*
- 7: sp mhc.*
- 8: sp organelle.*
- 9: sp phage.*
- 10: sp plant.*
- 11: sp rodent.*
- 12: sp virus.*
- 13: sp vertebrate.*
- 14: sp unclassified.*
- 15: sp virus.*
- 16: sp bacterioph.*
- 17: sp archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	73.4	291	16	Q98FS7
2	46	71.9	766	6	Q9N1R8
3	45	70.3	383	10	Q9S102
4	45	70.3	482	16	Q9KAQ6
5	43	67.2	538	5	Q9VGE6
6	43	67.2	570	5	Q17698
7	43	67.2	575	5	Q9VGE5
8	43	67.2	947	5	Q8SYA1
9	43	67.2	1218	5	Q9V8R6
10	42	65.6	176	17	Q8TP13
11	42	65.6	290	15	Q9YNA2
12	42	65.6	291	15	Q9YN99
13	42	65.6	293	10	O49488
14	42	65.6	374	10	O81798
15	42	65.6	392	10	Q9SVA3
16	42	65.6	442	12	Q91HI7

17	42	65.6	519	4	Q9Y480
18	42	65.6	641	4	Q9N2X0
19	42	65.6	642	4	Q9Y6Y0
20	42	65.6	873	6	Q9SN66
21	42	65.6	874	15	Q9WR73
22	41.5	64.8	312	10	Q9AVF3
23	41	64.1	144	2	Q9R7Z8
24	41	64.1	188	2	O87030
25	41	64.1	514	10	Q8VWL8
26	41	64.1	635	16	Q9KQR4
27	41	64.1	672	16	Q910K3
28	41	64.1	808	2	O70021
29	40	62.5	305	5	Q8WST5
30	40	62.5	345	2	Q9180
31	40	62.5	345	16	Q53933
32	40	62.5	378	10	Q9M2B5
33	40	62.5	474	5	Q9WSV7
34	40	62.5	513	5	Q9SSK6
35	40	62.5	519	16	Q9A9X4
36	40	62.5	612	10	Q8SB55
37	39	60.9	109	12	Q91UW3
38	39	60.9	155	2	Q54791
39	39	60.9	158	2	Q9RFC8
40	39	60.9	176	16	Q8ZRW3
41	39	60.9	176	16	Q8Z9K1
42	39	60.9	176	16	Q8XA24
43	39	60.9	177	2	Q9X755
44	39	60.9	177	6	Q9GLF8
45	39	60.9	240	16	Q9CFF6

ALIGNMENTS

RESULT 1

Q98FS7	ID	Q98FS7	PRELIMINARY;	PRT;	291 AA.
AC	Q98FS7				
DT	01-OCT-2001	(TREMBLrel. 18, Created)			
DT	01-OCT-2001	(TREMBLrel. 18, Last sequence update)			
DE	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			
DE	Hypothetical protein mlr3636.				
GN	MLR3636.				
OS	Rhizobium loti (Mesorhizobium loti).				
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;				
OC	Phyllobacteriaceae; Mesorhizobium.				
OX	NCBI_TaxID=381;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MAFF303099;				
RX	MEDLINE=21082930; PubMed=1214968;				
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,				
RA	Matanabe A., Idesawa K., Ishikawa K., Kawashima K., Kimura T.,				
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,				
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,				
RA	Takeuchi C., Yamada M., Tabata S.,				
RT	*Complete genome structure of the nitrogen-fixing symbiotic bacterium				
RT	Mesorhizobium loti.*				
RL	DNA Res. 7:331-338(2000).				
DR	EMBL; AP003002; BAB50490.1; -				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 291 AA; 31162 MW; 3C6E651E33A79EE2 CFC64;				

Query Match 73.4%; Score 47; DB 16; Length 291;
Best Local Similarity 70.0%; Pred. No. 3.3;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY

1 WYDPLTKLWL 10

Db 22 WFAPLTSUWL 31

RESULT 2

Q9N1R8 ID Q9N1R8 PRELIMINARY; PRT; 766 AA.
AC Q9N1R8; MEDLINE=2039162; PubMed=10933716;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE POL.
GN POL.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2039162; PubMed=10933716;
RA Palmarini M., Hallwirth C., York D., Murgia C., de Oliveira T.,
RA Spencer T., Fan H.;
RT "Molecular cloning and functional analysis of three type D endogenous
retroviruses of sheep reveal a different cell tropism from that of the
highly related exogenous Jaagsiekte sheep retrovirus.";
RL J. Virol. 74:8065-8076(2000).
DR EMBL; AF153615; AAP29458.1; -;
DR InterPro; IPR003308; Integrase_Zn.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; RVTse.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 766 AA; 86948 MW; 0CC13CBED56B399 CRC64;

Query Match 71.9%; Score 46; DE 6; Length 766;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
| | | | | | | |
Db 720 WKDPLTNLW 728

RESULT 3
Q9SI02 ID Q9SI02 PRELIMINARY; PRT; 383 AA.
AC Q9SI02; MEDLINE=20083487; PubMed=10617187;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE At2g22030 protein (Hypothetical 43.5 kDa protein).
GN At2G22030.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20083487; PubMed=10617187;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.B.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Smerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007232; AAD25821.1; -;
DR EMBL; AC007019; AM15347.1; -;
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01344; Kelch; 3.
DR SMART; SM00256; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 383 AA; 43474 MW; 23C6E99C913FED71 CRC64;

Query Match 70.3%; Score 45; DE 10; Length 383;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
| | | | | | | |
Db 288 WYDPRDKVM 296

RESULT 4
Q9KAQ6 ID Q9KAQ6 PRELIMINARY; PRT; 482 AA.
AC Q9KAQ6; MEDLINE=20512582; PubMed=11058132;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Hypothetical protein BH2231.
GN BH2231.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OC NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001514; BAB05950.1; -;
DR InterPro; IPR001173; Glycos transf 2.
DR Pfam; PF00535; Glycos transf 2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 482 AA; 54881 MW; CF151B8CF89824D CRC64;

Query Match 70.3%; Score 45; DE 16; Length 482;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
| | | | | | | |
Db 443 WYRPLTVLW 451

RESULT 5
Q9VGE6 ID Q9VGE6 PRELIMINARY; PRT; 538 AA.
AC Q9VGE6;
DT 01-MAY-2000 (Tremblrel. 13, Created)

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DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE CG3571 protein.
GN CG3571.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
(1)
RN RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B., Kohira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasbo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy K., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Spier E., Spradling A.C., Stempleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Wooley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EKBL; AE003694; AAF54738.1; -.
DR FlyBase; FBgn0037978; CG3571.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SMO0225; BTB; 1.
DR PROSITE; PS50097; BTB; 1.
SQ SEQUENCE 538 AA; 60427 MW; 93675C9A5726EBBF CRC64;

Query Match 57.2%; Score 43; DB 5; Length 538;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9
Db 275 YDPLTKW 282
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|||||

RESULT 6
O17698

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ID O17698 PRELIMINARY; PRT; 570 AA.
AC O17698;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE C53A5.6 protein.
GN C53A5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
(1)
RN RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B., Kohira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasbo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy K., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Spier E., Spradling A.C., Stempleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Wooley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EKBL; AE003694; AAF54738.1; -.
DR FlyBase; FBgn0037978; CG3571.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SMO0225; BTB; 1.
DR PROSITE; PS50097; BTB; 1.
SQ SEQUENCE 570 AA; 63294 MW; 58B5E1BE24FBA0F5 CRC64;

Query Match 57.2%; Score 43; DB 5; Length 570;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKLW 9
Db 492 YDPLTKSW 499
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|||||

RESULT 7
Q9VGES
ID Q9VGES PRELIMINARY; PRT; 575 AA.
AC Q9VGES;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE CG3571 protein (Lb42169P).
GN CG3571.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
(1)
RN RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E.,
RA Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Nuno J., Pacleb J., Paragas V., Park S.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; A0003694; AAP54737.1; -.
DR ENBL; AY001688; AAL49310.1; -.
DR FlyBase; FBgn0037978; CG3571.
DR InterPro; IPR00210; BTB_POZ.
DR InterPro; IPR001788; Kelch.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF01344; Kelch; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS00097; BTB; 1.
SQ SEQUENCE 575 AA; 64883 MW; 608F3BE4A6FA3283 CRC64;

Query Match 67.2%; Score 43; DB 5; Length 575;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YDPLTKW 9
DB 312 YDPLTKW 319

RESULT 8
Q8SYAL PRELIMINARY; PRT; 947 AA.
AC Q8SYAL;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE RH10407p.
GN CS7097.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Nephroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

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RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY01688; AAL49310.1; -.
SQ SEQUENCE 947 AA; 105224 MW; 814262CBD95FF56D CRC64;

Query Match 67.2%; Score 43; DB 5; Length 947;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WDPLTKW 10
DB 729 WDPLTKW 738

RESULT 9
Q9V8R6 PRELIMINARY; PRT; 1218 AA.
AC Q9V8R6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CG7097 protein.
GN CG7097.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Nephroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan X.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

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RL Science 287:2185-2195(2000).
 DR EMBL; AF003796; AAF57595.1; -.
 DR HSSP; F24941; 1BUH.
 DR Flybase; FBgn0034421; CG7097.
 DR InterPro; IPR001180; Citron.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00780; CNH; 1.
 DR Pfam; PF00669; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00336; CNH; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 1218 AA; 132395 MW; 78A7AF880CEBC8 CRC64;

Query Match 67.2%; Score 43; DB 5; Length 1218;
 Best Local Similarity 70.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 |||||
 DB 1000 WYDPLNKFML 1009

RESULT 10

QSTP13 PRELIMINARY; PRT; 176 AA.
 AC QSTP13;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Predicted protein.
 GN MA2114.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grubbs D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
 RA Pritchett M., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Metcalf W.W., Birren B.
 RA "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity."
 RL Genome Res. 12:532-542(2002).
 KW EMBL; AE010898; AAM05512.1; -.
 KW Complete proteome.
 SQ SEQUENCE 176 AA; 20158 MW; 6E257BDC471F2027 CRC64;

Query Match 65.6%; Score 42; DB 17; Length 176;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 9
 |||||
 DB 105 WYDPLTKLWL 113

RESULT 11

QSTP13 PRELIMINARY; PRT; 290 AA.
 AC QSTP13;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Predicted protein.
 GN MA2114.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grubbs D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
 RA Pritchett M., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Metcalf W.W., Birren B.
 RA "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity."
 RL Genome Res. 12:532-542(2002).
 KW EMBL; AE010898; AAM05512.1; -.
 KW Complete proteome.
 SQ SEQUENCE 176 AA; 20158 MW; 6E257BDC471F2027 CRC64;

AC Q9YNA2;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Reverse transcriptase (Fragment).
 GN GAG-POL OR POL.
 OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)
 OS (JSRV).
 OC Viruses; Retrovirus; Retroviridae; Retroviridae; Betaretrovirus.
 OX NCBI_TaxID=11746;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JS7;
 RX MEDLINE=99296727; PubMed=10366570;
 RA Bai J., Bishop J.V., Carlson J.O., Demartini J.C.;
 RT "Sequence comparison of JSRV with endogenous proviruses: envelope
 RT genotypes and a novel ORF with similarity to a G-protein-coupled
 RT receptor."
 RL Virology 258:333-343(1999).
 CC -1- PFM: SPECIFIC ENZYMMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
 CC (BY SIMILARITY).
 DR EMBL; Y18301; CAA77113.1; -.
 DR InterPro; IPR001037; Integrase_C.
 DR InterPro; IPR003308; Integrase_Zn.
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00552; Integrase; 1.
 DR Pfam; PF02022; Integrase_Zn; 1.
 DR Pfam; PF00665; rve; 1.
 KW Endonuclease; Hydrolase; Nucleosidyltransferase; Polyprotein;
 KW RNA-directed DNA polymerase.
 FT NON-TER
 SQ SEQUENCE 290 AA; 33190 MW; C33D2BD84022210 CRC64;
 Query Match 65.6%; Score 42; DB 15; Length 290;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 9
 |||||
 DB 229 WKDPFTNLW 237

RESULT 12
 Q9YNA2 PRELIMINARY; PRT; 291 AA.
 AC Q9YNA2;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Reverse transcriptase (Fragment).
 GN GAG-POL OR POL.
 OS Sheep pulmonary adenomatosis virus (Jaagsiekte sheep retrovirus)
 OS (JSRV).
 OC Viruses; Retrovirus; Retroviridae; Retroviridae; Betaretrovirus.
 OX NCBI_TaxID=11746;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JS7;
 RX MEDLINE=99296727; PubMed=10366570;
 RA Bai J., Bishop J.V., Carlson J.O., Demartini J.C.;
 RT "Sequence comparison of JSRV with endogenous proviruses: envelope
 RT genotypes and a novel ORF with similarity to a G-protein-coupled
 RT receptor."
 RL Virology 258:333-343(1999).
 CC -1- PFM: SPECIFIC ENZYMMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
 CC (BY SIMILARITY).
 DR EMBL; Y18301; CAA77113.1; -.
 DR InterPro; IPR001037; Integrase_C.
 DR InterPro; IPR003308; Integrase_Zn.
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00552; Integrase; 1.
 DR Pfam; PF02022; Integrase_Zn; 1.
 DR Pfam; PF00665; rve; 1.

KW Endonuclease; Hydrolase; Nucleotidyltransferase; Polyprotein;
KW RNA-directed DNA polymerase.
FT NON_TER 1
SQ SEQUENCE 291 AA; 3332 MW; 34912961BEDEB4FB CRC64;

Query Match 55.6%; Score 42; DB 15; Length 291;
Best Local Similarity 56.7%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
Db 230 WKDFTNLW 238

RESULT 13
O49488 PRELIMINARY; PRT; 293 AA.
AC O49488;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 33.4 kDa protein.
GN F28A23.70 OR AT4G34170
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Weichselgartner M., Partmann B., Granderath K., Dauner D.,
RA Herzl A., Neumann S., Hoheisel J., Jesse T., Heijnen L., Vos P.,
RA Mewes H.W., Mayer K., Schueller C.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Weichselgartner M., Partmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021961; CAB17555.1; -.
DR EMBL; AL161585; CAB80134.1; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01344; Kelch; 2.
DR SMART; SM00256; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 293 AA; 33448 MW; 50499260E168800E CRC64;

Query Match 55.6%; Score 42; DB 10; Length 293;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 9
Db 244 WYDPERVW 252

RESULT 14
O81798 PRELIMINARY; PRT; 374 AA.
ID O81798;
AC O81798;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Putative polygalacturonase (fragment).
GN F8D20.180 OR AT4G35670.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Koetter P., Hempel S., Entian K.-D., Hoheisel J., Jesse T.,
RA Heijnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
(POLYGALACTURONASES).
DR EMBL; AL031135; CAB20037.1; -.
DR EMBL; AL161587; CAB80283.1; -.
DR InterPro; IPR000743; GH28.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR PROSITE; PS00502; POLYGALACTURONASE; 1.
KW Cell wall; Glycosidase; Hydrolase; Signal.
FT NON_TER 1
SQ SEQUENCE 374 AA; 39884 MW; 3B86DB19DFB1ACB9 CRC64;

Query Match 65.6%; Score 42; DB 10; Length 374;
Best Local Similarity 40.0%; Pred. No. 30;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYDPLTKLW 10
Db 91 WSDPISRMWI 100

RESULT 15
Q8SVA3 PRELIMINARY; PRT; 392 AA.
ID Q8SVA3;
AC Q8SVA3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hypothetical 44.3 kDa protein.
GN F23K16.180 OR AT4G39550.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078620; CAB44690.1; -.
DR EMBL; AL161595; CAB80618.1; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001798; Kelch.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF01344; Kelch; 2.

DR SMART; SMO0256; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 392 AA; 44269 MW; 1EE507551D61FB7B CRC64;
Query Match 65.6%; Score 42; DB 10; Length 392;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WYDPLTKLW 9
Db 297 WYDTPARLW 305

Search completed: May 24, 2003, 17:12:43
Job time : 27 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 17:00:41 ; Search time 31 Seconds
(without alignments)
42.984 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDELTKLWL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002:**
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	10	23	ABJ00977 B lymphocyte affin
2	64	100.0	10	23	ABJ00997 B lymphocyte stimu
3	64	100.0	10	23	ABG33838 B lymphocyte stimu
4	64	100.0	10	23	ABG33859 B lymphocyte stimu
5	64	100.0	12	23	ABJ00996 B lymphocyte stimu
6	64	100.0	12	23	ABG33858 B lymphocyte stimu
7	64	100.0	13	23	ABJ00980 B lymphocyte affin
8	64	100.0	13	23	ABG33841 B lymphocyte stimu
9	64	100.0	14	23	ABJ00727 B lymphocyte affin
10	64	100.0	14	23	ABJ00728 B lymphocyte affin

11	64	100.0	14	23	ABJ00729 B lymphocyte affin
12	64	100.0	14	23	ABJ00730 B lymphocyte affin
13	64	100.0	14	23	ABJ00731 B lymphocyte affin
14	64	100.0	14	23	ABJ00732 B lymphocyte affin
15	64	100.0	14	23	ABJ00733 B lymphocyte affin
16	64	100.0	14	23	ABJ00734 B lymphocyte affin
17	64	100.0	14	23	ABJ00735 B lymphocyte affin
18	64	100.0	14	23	ABJ00736 B lymphocyte affin
19	64	100.0	14	23	ABJ00737 B lymphocyte affin
20	64	100.0	14	23	ABJ00738 B lymphocyte affin
21	64	100.0	14	23	ABJ00739 B lymphocyte affin
22	64	100.0	14	23	ABJ00740 B lymphocyte affin
23	64	100.0	14	23	ABJ00741 B lymphocyte affin
24	64	100.0	14	23	ABJ00742 B lymphocyte affin
25	64	100.0	14	23	ABJ00743 B lymphocyte affin
26	64	100.0	14	23	ABJ00744 B lymphocyte affin
27	64	100.0	14	23	ABJ00745 B lymphocyte affin
28	64	100.0	14	23	ABJ00746 B lymphocyte affin
29	64	100.0	14	23	ABJ00747 B lymphocyte affin
30	64	100.0	14	23	ABJ00748 B lymphocyte affin
31	64	100.0	14	23	ABJ00749 B lymphocyte affin
32	64	100.0	14	23	ABJ00750 B lymphocyte affin
33	64	100.0	14	23	ABJ00751 B lymphocyte affin
34	64	100.0	14	23	ABJ00752 B lymphocyte affin
35	64	100.0	14	23	ABJ00753 B lymphocyte affin
36	64	100.0	14	23	ABJ00754 B lymphocyte affin
37	64	100.0	14	23	ABJ00755 B lymphocyte affin
38	64	100.0	14	23	ABJ00756 B lymphocyte affin
39	64	100.0	14	23	ABJ00757 B lymphocyte affin
40	64	100.0	14	23	ABJ00758 B lymphocyte affin
41	64	100.0	14	23	ABJ00759 B lymphocyte affin
42	64	100.0	14	23	ABJ00760 B lymphocyte affin
43	64	100.0	14	23	ABJ00761 B lymphocyte affin
44	64	100.0	14	23	ABJ00762 B lymphocyte affin
45	64	100.0	14	23	ABJ00763 B lymphocyte affin

ALIGNMENTS

RESULT 1

ABJ00977

ID ABJ00977 standard; Peptide; 10 AA.

XX

AC ABJ00977;

DT

XX 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library core peptide.

XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antasthmatic; antiallergic; thyromimetic; antinaemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.

OS Unidentified.

XX WO200216411-A2.

PN

XX 28-FEB-2002.

XX

XX 17-AUG-2001; 2001WO-US25850.

XX

XX 18-AUG-2000; 2000US-226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

PI

XX WPI; 2002-499775/53.
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide -
 XX Example 11; Page 377; 387pp; English.
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 64; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 DB 1 WYDPLTKLWL 10
 RESULT 2
 ABJ00997
 ID ABJ00997 standard; Peptide; 10 AA.
 AC ABJ00997;
 XX 05-SEP-2002 (first entry)
 DT B lymphocyte stimulator protein binding peptide #168.
 DE B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX Unidentified.
 OS WO200216411-A2.
 XX 28-FEB-2002.
 XX 17-AUG-2001; 2001WO-US25850.
 XX 18-AUG-2000; 2000US-226700P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Beltzer JP, Potter DM, Fleming TJ, Rosen CA;
 XX WPI; 2002-499775/53.
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide -
 XX Claim 71; Page 236; 387pp; English.

XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of BlyS binding polypeptide.
 CC The BlyS binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of haematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX Sequence 10 AA;
 SQ Query Match 100.0%; Score 64; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0004;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 DB 1 WYDPLTKLWL 10
 RESULT 3
 ABG33838
 ID ABG33838 standard; Peptide; 10 AA.
 AC ABG33838;
 XX 15-JUL-2002 (first entry)
 DT B lymphocyte stimulator (BlyS) binding peptide #414.
 DE B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KW BlyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX Synthetic.
 OS WO200216412-A2.
 XX 28-FEB-2002.
 XX 17-AUG-2001; 2001WO-US25891.
 XX 18-AUG-2000; 2000US-226489P.
 XX (DYAX-) DYAX CORP.
 XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
 XX WPI; 2002-351647/38.
 XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating BlyS or BlyS-like polypeptide comprises a specified amino
 PT acid sequence -
 XX Claim 4; Page 97; 269pp; English.
 XX The invention relates to a B lymphocyte stimulator (BlyS) binding
 CC polypeptide. BlyS binding peptides bind BlyS or BlyS-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of BlyS in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue
 CC culture or other source containing BlyS or BlyS-like polypeptides. The
 CC biological fluids include sera, plasma, lymph, blood, blood fraction,
 CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent BlyS binding peptides of the invention.

XX SQ Sequence 10 AA;
Query Match 100.0%; Score 64; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
Db 1 WYDPLTKLWL 10

RESULT 4
ABG33859
ID ABG33859 standard; Peptide; 10 AA.
XX AC ABG33859;
XX DT 15-JUL-2002 (first entry)
XX DE B Lymphocyte Stimulator (BlyS) binding peptide #433.
XX KW B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
XX KW BlyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
XX KW synovial fluid; saliva; mucus.
XX OS Synthetic.
XX PN WO200216412-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US25891.
XX PR 18-AUG-2000; 2000US-226489P.
XX PA (DYAX-) DYAX CORP.
XX PI Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
XX WPI; 2002-351647/38.
XX PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating BlyS or BlyS-like polypeptide comprises a specified amino
PT acid sequence -
XX PS Claim 8; Page 98; 269pp; English.
XX CC The invention relates to a B Lymphocyte Stimulator (BlyS) binding
CC polypeptide. BlyS binding peptides bind BlyS or BlyS-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of BlyS in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing BlyS or BlyS-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucus. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent BlyS binding peptides of the invention.
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 64; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
Db 1 WYDPLTKLWL 10

RESULT 5
ABJ00996
ID ABJ00996 standard; Peptide; 12 AA.
XX AC ABJ00996;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte stimulator protein binding peptide #167.
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antinaeemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX OS Unidentified.
XX PN WO200216411-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-US25850.
XX PR 18-AUG-2000; 2000US-226700P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX WPI; 2002-499775/53.
XX PT The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide -
XX PS Claim 71; Page 236; 387pp; English.
XX CC The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX SQ Sequence 12 AA;
Query Match 100.0%; Score 64; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
| | | | |
Db 1 WYDPLTKLWL 10

RESULT 6
ABG33858
ID ABG33858 standard; Peptide; 12 AA.
XX AC ABG33858;
XX DT 15-JUL-2002 (first entry)
XX DE B Lymphocyte Stimulator (BlyS) binding peptide #432.

XX B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX Synthetic.
 OS
 XX WO200216412-A2.
 PN
 XX 28-FEB-2002.
 PD
 XX 17-AUG-2001; 2001WO-US25891.
 PF
 XX 18-AUG-2000; 2000US-226489P.
 XX (DYAX-) DYAX CORP.
 PA
 XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
 PI WPI; 2002-351647/38.
 XX
 DR New B-lymphocyte stimulator binding polypeptide useful in detecting or
 XX isolating Blys or Blys-like polypeptide comprises a specified amino
 PT acid sequence -
 PT
 XX
 XX Claim 8; Page 98; 269pp; English.
 PS
 XX The invention relates to a B Lymphocyte Stimulator (Blys) binding
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue
 CC culture or other source containing Blys or Blys-like polypeptides. The
 CC biological fluids include sera, plasma, lymph, blood, blood fractions,
 CC urine, synovial fluid, spinal fluid, saliva and mucus. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent Blys binding peptides of the invention.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 100.0%; Score 64; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 DB 1 WYDPLTKLWL 10
 |||||
 RESULT 7
 ABJ00980
 ID ABJ00980 standard; Peptide; 13 AA.
 XX
 AC ABJ00980;
 XX
 XX 05-SEP-2002 (first entry)
 DT
 XX B lymphocyte affinity maturation library peptide#253.
 DE
 XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiasthmatic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 XX WO200216411-A2.
 PN

XX 28-FEB-2002.
 PD
 XX 17-AUG-2001; 2001WO-US25850.
 PF
 XX 18-AUG-2000; 2000US-226700P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 PI WPI; 2002-499775/53.
 DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
 XX administering B lymphocyte stimulator binding polypeptide -
 PT
 XX
 XX Example 11; Page 220; 387pp; English.
 PS
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 100.0%; Score 64; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00052;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WYDPLTKLWL 10
 DB 1 WYDPLTKLWL 10
 |||||
 RESULT 8
 ABG33841
 ID ABG33841 standard; Peptide; 13 AA.
 XX
 AC ABG33841;
 XX
 XX 15-JUL-2002 (first entry)
 DT
 XX B Lymphocyte Stimulator (Blys) binding peptide #417.
 DE
 XX B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX
 OS Synthetic.
 XX
 XX WO200216412-A2.
 PN
 XX 28-FEB-2002.
 PD
 XX 17-AUG-2001; 2001WO-US25891.
 PF
 XX 18-AUG-2000; 2000US-226489P.
 PR
 XX (DYAX-) DYAX CORP.
 PA
 XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
 PI WPI; 2002-351647/38.
 DR
 XX

PT New B-lymphocyte stimulator binding polypeptide useful in detecting or
PT isolating BlyS or BlyS-like polypeptide comprises a specified amino
XX acid sequence -
PS Claim 7; Page 94; 269pp; English.
XX The invention relates to a B lymphocyte stimulator (BlyS) binding
CC polypeptide. BlyS binding peptides bind BlyS or BlyS-like proteins
CC reversibly or irreversibly. The binding peptides are used in detection,
CC isolation and/or purification of BlyS in a solution such as water or a
CC buffer solution, as well as any fluid and/or cell obtained from an
CC individual biological fluid, body tissue, body cell, cell line, tissue
CC culture or other source containing BlyS or BlyS-like polypeptides. The
CC biological fluids include sera, plasma, lymph, blood, blood fraction,
CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
CC ABG33852-33862 represent BlyS binding peptides of the invention.
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 64; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | |
Db 1 WYDPLTKLWL 10

RESULT 9
ABJ00727
ID ABJ00727 standard; Peptide; 14 AA.

XX AC ABJ00727;

XX 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #1.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX

OS Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US25850.

XX 18-AUG-2000; 2000US-226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide -

XX Claim 70; Page 236; 387pp; English.

XX The present invention relates to the treatment, prevention or

CC amelioration of a disease or disorder associated with: aberrant B

CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells

CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of hematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | |
Db 3 WYDPLTKLWL 12

RESULT 10

ABJ00728
ID ABJ00728 standard; Peptide; 14 AA.

XX AC ABJ00728;

XX 05-SEP-2002 (first entry)

DE B lymphocyte affinity maturation library peptide #2.

XX B lymphocyte stimulator protein binding protein; BlyS; immune disease;
KW allergy; proliferative disease; infectious disease; arteriosclerosis;
KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX

OS Unidentified.

XX WO200216411-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-US25850.

XX 18-AUG-2000; 2000US-226700P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;

XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B lymphocyte stimulator binding polypeptide -

XX Claim 70; Page 214; 387pp; English.

XX The present invention relates to the treatment, prevention or

CC amelioration of a disease or disorder associated with: aberrant B

CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells

CC of haematopoietic origin; or proliferative disease; and reducing,
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of BlyS binding polypeptide.
CC The BlyS binding polypeptides are used in the treatment, prevention or

CC amelioration of diseases such as immune system diseases, proliferative

CC diseases, diseases of cells of hematopoietic origin, graft rejection,

CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,

CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide

XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 64; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 DB 3 WYDPLTKLWL 12

RESULT 11
 ABJ00729
 ID ABJ00729 standard; Peptide; 14 AA.
 XX
 AC ABJ00729;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide #3.
 XX
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antitumour; anti-HIV;
 KW antiaesthetic; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 XX WO200216411-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US25850.
 XX
 XX 18-AUG-2000; 2000US-226700P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX WPI; 2002-499775/53.
 XX
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 XX administering B lymphocyte stimulator binding polypeptide .
 XX
 XX Claim 70; Page 214; 387pp; English.
 XX
 XX The present invention relates to the treatment, prevention or
 XX amelioration of a disease or disorder associated with: aberrant B
 XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 XX of haematopoietic origin; or proliferative disease; and reducing,
 XX inhibiting or stimulating immunoglobulin production, B cell proliferation
 XX and graft rejection involving administration of BlyS binding polypeptide.
 XX The BlyS binding polypeptides are used in the treatment, prevention or
 XX amelioration of diseases such as immune system diseases, proliferative
 XX diseases, diseases of cells of haematopoietic origin, graft rejection,
 XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 XX neurodegenerative diseases. The present sequence is a B lymphocyte
 XX stimulator protein binding peptide

XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 64; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 DB 3 WYDPLTKLWL 12

Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 DB 3 WYDPLTKLWL 12

RESULT 12
 ABJ00730
 ID ABJ00730 standard; Peptide; 14 AA.
 XX
 AC ABJ00730;
 XX
 DT 05-SEP-2002 (first entry)
 XX
 DE B lymphocyte affinity maturation library peptide #4.
 XX
 KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antitumour; antiarthritic;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiaesthetic; antiallergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX
 OS Unidentified.
 XX
 XX WO200216411-A2.
 XX
 XX 28-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US25850.
 XX
 XX 18-AUG-2000; 2000US-226700P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX WPI; 2002-499775/53.
 XX
 XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 XX administering B lymphocyte stimulator binding polypeptide -
 XX
 XX Claim 70; Page 214; 387pp; English.
 XX
 XX The present invention relates to the treatment, prevention or
 XX amelioration of a disease or disorder associated with: aberrant B
 XX lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
 XX of haematopoietic origin; or proliferative disease; and reducing,
 XX inhibiting or stimulating immunoglobulin production, B cell proliferation
 XX and graft rejection involving administration of BlyS binding polypeptide.
 XX The BlyS binding polypeptides are used in the treatment, prevention or
 XX amelioration of diseases such as immune system diseases, proliferative
 XX diseases, diseases of cells of haematopoietic origin, graft rejection,
 XX allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 XX hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 XX neurodegenerative diseases. The present sequence is a B lymphocyte
 XX stimulator protein binding peptide

XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 64; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
 DB 3 WYDPLTKLWL 12


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RESULT 13
ABJ00731
ID ABJ00731 standard; Peptide; 14 AA.
XX AC ABJ00731;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte affinity maturation library peptide #5.
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
XX KW dermatological; antinflammatory; cardiant; ophthalmological; uropathic;
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX OS Unidentified.
XX FN WO200216411-A2.
XX XX 28-FEB-2002.
XX PD 17-AUG-2001; 2001WO-US25850.
XX PF 18-AUG-2000; 2000US-226700P.
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX PI WPI; 2002-499775/53.
XX DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX PT administering B Lymphocyte stimulator binding polypeptide -
XX PS Claim 70; Page 214; 387pp; English.
XX CC The present invention relates to the treatment, prevention or
XX CC amelioration of a disease or disorder associated with: aberrant B
XX CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX CC of haematopoietic origin; or proliferative disease; and reducing,
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation
XX CC and graft rejection involving administration of BlyS binding polypeptide.
XX CC The BlyS binding polypeptides are used in the treatment, prevention or
XX CC amelioration of diseases such as immune system diseases, proliferative
XX CC diseases, diseases of cells of haematopoietic origin, graft rejection,
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX CC stimulator protein binding peptide
XX SQ Sequence 14 AA;
XX Query Match 100.0%; Score 64; DB 23; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00057;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12
RESULT 14
ABJ00732
ID ABJ00732 standard; Peptide; 14 AA.
XX AC ABJ00732;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte affinity maturation library peptide #7.
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
XX KW ischaemia; graft-versus-host disease; neurodegenerative disease;
XX KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
XX KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
XX KW antiasthmatic; antiallergic; thyromimetic; antianemic; haemostatic;
XX KW dermatological; antinflammatory; cardiant; ophthalmological; uropathic;
XX KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX OS Unidentified.
XX FN WO200216411-A2.
XX XX 28-FEB-2002.
XX PD 17-AUG-2001; 2001WO-US25850.
XX PF 18-AUG-2000; 2000US-226700P.
XX PR (HUMA-) HUMAN GENOME SCI INC.
XX PA Beltzer JP, Potter DM, Fleming TL, Rosen CA;
XX PI WPI; 2002-499775/53.
XX DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
XX PT administering B Lymphocyte stimulator binding polypeptide -
XX PS Claim 70; Page 214; 387pp; English.
XX CC The present invention relates to the treatment, prevention or
XX CC amelioration of a disease or disorder associated with: aberrant B
XX CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells
XX CC of haematopoietic origin; or proliferative disease; and reducing,
XX CC inhibiting or stimulating immunoglobulin production, B cell proliferation
XX CC and graft rejection involving administration of BlyS binding polypeptide.
XX CC The BlyS binding polypeptides are used in the treatment, prevention or
XX CC amelioration of diseases such as immune system diseases, proliferative
XX CC diseases, diseases of cells of haematopoietic origin, graft rejection,
XX CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
XX CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
XX CC neurodegenerative diseases. The present sequence is a B lymphocyte
XX CC stimulator protein binding peptide
XX SQ Sequence 14 AA;
XX Query Match 100.0%; Score 64; DB 23; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00057;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WYDPLTKLWL 10
DB 3 WYDPLTKLWL 12
RESULT 15
ABJ00733
ID ABJ00733 standard; Peptide; 14 AA.
XX AC ABJ00733;
XX DT 05-SEP-2002 (first entry)
XX DE B lymphocyte affinity maturation library peptide #7.
XX KW B lymphocyte stimulator protein binding protein; BlyS; immune disease;
XX KW allergy; proliferative disease; infectious disease; arteriosclerosis;
XX KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;

```

KW ischaemia; graft-versus-host disease; neurodegenerative disease;
KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
KW antidiabetic; antiallergic; thyrostatic; antineoplastic; haemostatic;
KW dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;
KW antidiabetic; antithyroid; antidepressant; hepatotropic.
XX
OS Unidentified.
XX
XX WO200216411-A2.
PN
XX
PD 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US25850.
PP
XX
XX 18-AUG-2000; 2000US-226700P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
PI WPI; 2002-499775/53.
XX
XX
DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
PT administering B Lymphocyte stimulator binding polypeptide -
PT
XX
XX Claim 70; Page 214; 387pp; English.
XX
XX The present invention relates to the treatment, prevention or
CC amelioration of a disease or disorder associated with: aberrant B
CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
CC of haematopoietic origin; or proliferative disease; and reducing
CC inhibiting or stimulating immunoglobulin production, B cell proliferation
CC and graft rejection involving administration of Blys binding polypeptide.
CC The Blys binding polypeptides are used in the treatment, prevention or
CC amelioration of diseases such as immune system diseases, proliferative
CC diseases, diseases of cells of haematopoietic origin, graft rejection,
CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
CC hypergammaglobulinemia, blood clotting disorders, ischaemia, and
CC neurodegenerative diseases. The present sequence is a B lymphocyte
CC stimulator protein binding peptide
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 23; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | |
Db 3 WYDPLTKLWL 12

Search completed: May 24, 2003, 17:11:22
Job time : 32 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 17:12:46 ; Search time 16.5 Seconds
(without alignments)
60.105 Million cell updates/sec

Title: US-09-932-613-457

Perfect score: 64

Sequence: 1 WYDPLTKLWL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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3: /cgm2_6/ptodata/2/pubpaa/US06 NEW PUB.pap.*
4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
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9: /cgm2_6/ptodata/2/pubpaa/US09 NEW PUB.pap.*
10: /cgm2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
11: /cgm2_6/ptodata/2/pubpaa/US10 NEW PUB.pap.*
12: /cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
13: /cgm2_6/ptodata/2/pubpaa/US60 NEW PUB.pap.*
14: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query March	Length	ID	Description
1	64	100.0	10	9	US-09-932-613-436
2	64	100.0	10	9	US-09-932-613-457
3	64	100.0	12	9	US-09-932-613-456
4	64	100.0	13	9	US-09-932-613-439
5	64	100.0	14	9	US-09-932-613-186
6	64	100.0	14	9	US-09-932-613-187
7	64	100.0	14	9	US-09-932-613-188
8	64	100.0	14	9	US-09-932-613-189
9	64	100.0	14	9	US-09-932-613-190
10	64	100.0	14	9	US-09-932-613-191
11	64	100.0	14	9	US-09-932-613-192
12	64	100.0	14	9	US-09-932-613-193
13	64	100.0	14	9	US-09-932-613-194
14	64	100.0	14	9	US-09-932-613-195
15	64	100.0	14	9	US-09-932-613-196
16	64	100.0	14	9	US-09-932-613-197
17	64	100.0	14	9	US-09-932-613-198
18	64	100.0	14	9	US-09-932-613-199
19	64	100.0	14	9	US-09-932-613-200

ALIGNMENTS

RESULT 1

US-09-932-613-436
; Sequence 436, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rozen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dlx-025.1 PCT; Dlx-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 436
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: core peptide of high affinity Blys binders
US-09-932-613-436

Query Match 100.0%; Score 64; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
| | | | | | | | | |
Db 1 WYDPLTKLWL 10

RESULT 2

US-09-932-613-457
; Sequence 457, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.

Sequence 201, App
Sequence 202, App
Sequence 203, App
Sequence 204, App
Sequence 205, App
Sequence 206, App
Sequence 207, App
Sequence 208, App
Sequence 209, App
Sequence 210, App
Sequence 211, App
Sequence 212, App
Sequence 213, App
Sequence 214, App
Sequence 215, App
Sequence 216, App
Sequence 217, App
Sequence 218, App
Sequence 219, App
Sequence 220, App
Sequence 221, App
Sequence 222, App
Sequence 223, App
Sequence 224, App
Sequence 225, App
Sequence 226, App

; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 457
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-457

Query Match 100.0%; Score 64; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00025; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
DB 1 WYDPLTKLWL 10

RESULT 3
US-09-932-613-456
; Sequence 456, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 456
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-456

Query Match 100.0%; Score 64; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0003; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
DB 1 WYDPLTKLWL 10

RESULT 4
US-09-932-613-439
; Sequence 439, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 439
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-439

Query Match 100.0%; Score 64; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
DB 1 WYDPLTKLWL 10

RESULT 5
US-09-932-613-186
; Sequence 186, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-186

Query Match 100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 WYDPLTKLWL 10
| | | | | | | | | |
DB 3 WYDPLTKLWL 12

RESULT 6
US-09-932-613-187
; Sequence 187, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 187
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-187

```
Query Match      100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 7
US-09-932-613-188
; Sequence 188, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-188

Query Match      100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 8
US-09-932-613-189
; Sequence 189, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 189
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-189

Query Match      100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12
```

```
Db 3 WYDPLTKLWL 12

RESULT 9
US-09-932-613-190
; Sequence 190, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 190
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-190

Query Match      100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 10
US-09-932-613-191
; Sequence 191, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 191
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-191

Query Match      100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 11
US-09-932-613-192
; Sequence 192, Application US/09932613
; Publication No. US20030091565A1
```

GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-192

Query Match 100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 12

US-09-932-613-193
; Sequence 193, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-193

Query Match 100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 13

US-09-932-613-194
; Sequence 194, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 194
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-194

Query Match 100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 14

US-09-932-613-195
; Sequence 195, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 195
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-195

Query Match 100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDPLTKLWL 10
Db 3 WYDPLTKLWL 12

RESULT 15

US-09-932-613-196
; Sequence 196, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 14

: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-196

Query Match 100.0%; Score 64; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYDELTKLWL 10
Db 3 WYDELTKLWL 12

Search completed: May 24, 2003, 17:23:36
Job time : 16.5 secs

```

> O <
O||O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

    -- Outline of search "seq448-iss" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
seq448 (AA) ID seq448 AA preliminary pattern
followed by
1 w o r e o r c o r l o r a o r r o r g o r s
2 y o r f o r e o r c o r n
2 d
2 p o r s o r t o r f o r l o r y o r c o r a
2 i t
2 k o r n o r q o r g o r r
2 l
2 w o r s o r t o r r o r c o r y o r k
2 l o r f o r v o r i o r h

Selected data banks and files:

Data bank : Issued_AA , all entries

    -- Output Parameters --

Format Options:
Nucleic acid code matching Exact No No
Find non-matching hits only No Sequence or key file No
Report key used Yes List of hits No
Note position of hit Yes Hit display Yes
Display full annotations Yes Name and annotations Yes
Sequence context 50

Run mode Batch
Time to start comparison now
Notify at end of run No

No hits found.

    -- Run Parameters --

    -- Search Statistics --

Times: CPU Total Elapsed
00:03:08.16 00:03:29.00

Number of sequences searched: 262643
Number of sequence hits: 0
Number of separate matches: 0
Number of sequence hits saved: 0

```



```
! FINDPATTERNS on pir:* allowing 0 mismatches
!      1 (W,E,K,C,L,A,R,G,S)(Y,F,E,C,N)D(P,S,T,F,L,Y,C,A)LT(K,N,Q,G,R)L(W,S,T,R,C,Y,K)

S36713 ck: 1621 len: 837 ! CCR4 protein - yeast (Saccharomyces cerevisiae)
(W,E,K,C,L,A,R,G,S)(Y,F,E,C,N)D(P,S,T,F,L,Y,C,A)LT(K,N,Q,G,R)L(W,S,T,R,C,Y,K)
(K)(Y)D(F)LT(R)L(Y)(L)
355: SANIF KYDFLTRLYL NGNSL
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Databases searched:
NBRF, Release 73.0, Released on 16Aug2002, Formatted on 20Aug2002

Total finds:	1
Total length:	96,134,422
Total sequences:	283,224
CPU time:	14:19.57

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!!SEQUENCE_LIST 1.0
! FINDPATTERNS on pir:* allowing 0 mismatches
!      1 (W,E,K,C,L,A,R,G,S)(Y,F,E,C,N)D(P,S,T,F,L,Y,C,A)IT(K,N,Q,G,R)L(W,S,T,R,C,Y,K)
PIR2:S36713      ck: 1621 len: 837 finds: 1 ! CCR4 protein - yeast (Saccharo
\\End of list

Databases searched:
  NBRF, Release 73.0, Released on 16Aug2002, Formatted on 20Aug2002
    Total finds: 1
    Total length: 96,134,422
    Total sequences: 283,224
    CPU time: 15:06.09
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!!AA SEQUENCE 1.0
P1:S36713 - CCR4 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YAL021c
C:Species: Saccharomyces cerevisiae
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Oct-1999
C:Accession: S36713; S31286
R:Oueltette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.;
Fortin, N.; Delaney, S.; Barton, A.; Kaback, D.B.; Bussey, H.
submitted to the EMBL Data Library, January 1993
A:Description: Sequencing of Chromosome I from Saccharomyces cerevisiae:
analysis of a 32 kilobase region between the LTEL and SPO7 genes.
A:Reference number: S36711
A:Accession: S36713
A:Molecule type: DNA
A:Residues: 1-837 <OUE>
A:Cross-references: EMBL:L05146; NID:g171851; PIDN:AAC04936.1; PID:g171854;
MIPS:YAL021c
R:Malvar, I.; Biron, R.W.; Kaback, D.B.; Denis, C.L.
Genetics 132, 951-962, 1992
A:Title: The CCR4 protein from Saccharomyces cerevisiae contains a leucine-rich
repeat region which is required for its control of ADH2 gene expression.
A:Reference number: S31286; MUID:93093455; PMID:1459446
A:Accession: S31286
A:Molecule type: DNA
A:Residues: 1-543, 'L', 545-802, 'E', 804-837 <VAL>
A:Cross-references: EMBL:S0459; NID:g261566; PIDN:AB24455.1; PID:g261567
C:Genetics:
A:Gene: SGD:CCR4; FUN27
A:Cross-references: SGD:S0000019; MIPS:YAL021c
A:Map position: 1L
C:Superfamily: leucine-rich alpha-2-glycoprotein repeat homology
F:335-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:358-380/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:381-403/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:404-426/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:427-450/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

S36713 Length: 837 May 24, 2003 18:57 Type: P Check: 1621 ..
1 MNDFSLGYP NVGPQQQQQ QQQQHAGLIG KGTPNALQQQ LHMNQLTGIP
51 PPGLMNNSDV HTSSNNNSRQ LLDQLANGNA NMLNMNMDNN NNNNNNNNN
101 NNNGGSGVM MNASTAAVNS IGMVPTVGT P VNINVNASNP LLHPHLDPS
151 LLNDFIWLKQ LHLAAVAQS LGQPNYARQ NAMKKYLATQ QAQAAQQAAQ
201 QQAQQQVPGP FPGPQAAPP ALOPTDFQOS HIAEASKSLV DCTKQALMEM
251 ADTLTDSKTA KKQPTGDS T PSCTATNSAV STPLTPKIEL FANGKDEANQ
301 ALLQHKLSQ YSIDEDDIE NRMVMPKDSK YDDQLWHALD LSNLQIFNIS
351 ANIPKYDFLT RLYLNGNSLT ELPAEIKNLS NLRVLDLSHN RLTSPLPAELG
401 SCFQLKYTFV FDNMVTTLPW EFGNLCNLQF LGVEGNPLEK QFLKILTEKS
451 VTGLIFYLRD NRPIPLPHE RRIENTDG EPQREYDSLQ QSTEHLATDL
501 AKRTFTVLSY NTLQHYATP KMRYTPSWA LSWDYERNKL KEQILSYDSD
551 LLLQVEVESK TFEEYVYVPLL DXHGYTGIFH AKARAKTMHS KDSKKVDGCC
601 IFFKEDQFKL ITKDAMDFSG ANMKHKFKQR TEDYLNRAVN KDNVALFLKL
651 QHIPSGDTIW AVTHLHWD P KNDVKTQV GVLLDHLDEL LKBETSHNFR
701 QDIKKFPVLI CGDFNSYNS AVYELINTGR VQIHQEGNGR DFGYMSEKNE
751 SHNLAKSSY NCIGELPFTN FTFSFTDVID YIWFSTHALR VRGLLGEVDP
801 EYVSKFICFP NDKFPSDHP LLARFEMKT NTGSKKV

```

```
! FINDPATTERNS on swp:* allowing 0 mismatches
!      1 (W,E,K,C,L,A,R,G,S)(Y,F,E,C,N)D(P,S,T,F,L,Y,C,A)LT(K,N,Q,G,R)L(W,S,T,R,C,Y,K)

CIKA_BACTM ck: 5162 len: 1,215 ! Q45715 bacillus thuringiensis (subsp. morri
(L)(Y)D(F)LT(N)L(T)(I)
327: IRQPH LYDFLTNLT I YTRS

CCR4_YEAST ck: 1629 len: 837 ! P31384 saccharomyces cerevisiae (baker's ye
(W,E,K,C,L,A,R,G,S)(Y,F,E,C,N)D(P,S,T,F,L,Y,C,A)LT(K,N,Q,G,R)L(W,S
(K)(Y)D(F)LT(R)L(Y)(L)
355: SANIF KYDFLTRLYL NGNSL

Q9V363 ck: 3076 len: 407 ! Q9V363 drosophila melanogaster (fruit fly)
(W,E,K,C,L,A,R,G,S)(Y,F,E,C,N)D(P,S,T,F,L,Y,C,A)LT(K,N,Q,G,R)L(W,S
(A)(F)D(L)LT(N)L(C)(V)
329: ALKVT AFDLTNLCV ANISD
```

Databases searched:
SWISS-PROT, Release 40.3, Released on 9Aug2002, Formatted on 20Aug2002
SPTREMBL, Release 21.0, Released on 15Jun2002, Formatted on 28Jun2002

Total finds:	3
Total lengths:	247,523,443
Total sequences:	784,472
CPU time:	37:22.99

```
!!SEQUENCE LIST 1.0
! FINDPATTERNS on swp:* allowing 0 mismatches
!      1 (W,E,K,C,L,A,R,G,S)(Y,F,E,C,N)D(P,S,T,F,L,Y,C,A)LT(K,N,Q,G,R)L(W,S,T,R,C,Y,K)

SW:ClKA_BACTM      ck: 5162 len: 1,215 finds: 1 ! Q45715 bacillus thuringiensis
SW:CCR4_YEAST      ck: 1629 len: 837 finds: 1 ! P31384 saccharomyces cerevisia
SP_IN:Q9V363       ck: 3076 len: 407 finds: 1 ! Q9V363 drosophila melanogaster
\\End of list

Databases searched:
  SWISS-PROT, Release 40.3, Released on 9Aug2002, Formatted on 20Aug2002
  SPTREMBL, Release 21.0, Released on 15Jun2002, Formatted on 28Jun2002

Total finds: 3
Total length: 247,523,443
Total sequences: 784,472
CPU time: 39:44.64
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```

!!AA_SEQUENCE 1.0
ID_CIK_A_BACTM STANDARD; PRT; 1215 AA.
AC Q45715;
DT 30-MAY-2000 (Rel. 39, Created);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Peptidic crystal protein cryika (insecticidal delta-endotoxin
DE CRYIKA) (Crystaline endotoxin) (137 kDa crystal protein).
GN CRYIKA OR CRYIKA) OR CRYIK.
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1441;
RN [1];
RP SEQUENCE FROM N.A.
RX STRAIN=F190;
RX MEDLINE=96102856; PubMed=8586263;
RA Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
RT "Cloning of a novel crystal protein gene cryik from Bacillus
RT thuringiensis subsp. morrisoni";
RL FEMS Microbiol Lett. 134:159-164(1995).
CC -!- FUNCTION: PROMOTES COLLOIDSMOTIC LYSIS BY BINDING TO THE MIDGUT
CC EPITHELIAL CELLS OF INSECTS. SELECTIVELY TOXIC TO ARTOGEIA RAPAE
CC AND NOT ACTIVE ON PLUTELLA XYLOSTELLA.
CC -!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
CC SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
CC OF THE SPORE COAT.
CC -!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
CC N-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U28801; AAB00376.1;
CC HSP; P02965; 1C1V.
CC InterPro; IPR001170; Endotoxin.
CC Pfam; PF00555; endotoxin; 1.
CC Toxin; Sporulation.
KW Toxin; Sporulation.
SQ SEQUENCE 1215 AA; 137378 MW; 7CAF7A3311893D9B CRC64;

CIKA_BACTM Length: 1215 May 24, 2003 19:38 Type: P Check: 5162

1 MNSNRKNE INALSIPIV SNHSAQMDLS PDARIEDSLC VAEGNNIDPF
51 VSASTVQTGI SIAGRILGYL GVPPAGQLAS FYSPLVUGELW PGRDRPWEIF
101 MEHVEQIVRQ QQITDSVRT AIARLEGLGR GYRSYQQALE TWLDNRNDAR
151 SRSLIRERY ALELDITTAI PLFSIRNEEV PLMVVAQAA NLHLILLRDA
201 SLFGSEWGMs SADVNQYQOE QIRYTEEYSN HCVQWNTGL NLRGTTAET
251 WRYNQPRRD LTLGLDLVA LPSPYDRTY PIPITQALTR EYVTPNGVV
301 AGPNNSWFRN GASFAIENA IIRPHLYDF LTNLTITRR SQVGTIMML
351 WAGHRTFNR IGGTSEMY YGAINPVSV SDIPFVNRDV YRTVSLAGGL
401 GSLGIRYGL TRVDFDMIFR NEPDIVTGLF YHPGHAGIAT QVKQSDTELP
451 PETTEQPNYR AFSHLLSHIS MGPTTQDVPV VSWTHQSAD RNTINSRI
501 TQPLVKAHT LSGTTVVGK PGFTGGDILR RTSGGPFAPS NVNLDNLSQ
551 RYPARIYAS TTNRIYTVV AGERIFAGQF DKTWDAGAPL TFOSTSYATI
601 NTAFTPPERS SLLTIGADTF SSGNEVYVDR FELIQTATF EAESLERAR

```

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651 KAVNALFTST NPRGLKTDVT DYHIDQVSNL VECLSDERCL DKRELLSEV
701 KYAKRLSDER NLLQDPTFTS ISGQTDGWI GSTGISIQGG DDIFKENVVR
751 LPTVDCEVP TYLYKIDES QLKSYTRYQL RGYIEDSQDL EYILIRYNAK
801 HETLSVPGTE SPWPSSGVYP SGRGCEPNRC APRIENPDL DCSCRYGKCC
851 VHHSHHFLSD IDVGCTDLNE DLGWWVIFKI KTQDGHAKUG NLEFIEEKPL
901 LGKALSRVR AEKWRDKYE KLOETKRVY TEAKESVDAL FVDSQYDKLQ
951 ANTNIGIIRG ADKQVHRIR PYLSELPVIP SINAAIFEEL EGHIFKAYS
1001 YDARNVIKNG DFNGLSCWN VKGHVDVQON HHRSVLVLSE WEAEVSQKVR
1051 VCPDRGYILR VTAYKEGVE GCVTIHEFED NTDVLKFRNF VEEVEYPNNT
1101 VTCNDYTNQ SAEGSTDACN SYNRYEDGY ENRYEPNPSA PVNKTPTYEE
1151 GMYTDQGYN HCVSRGYRN HTPLPAGYVT LELEYFPETE QVWIEIGETE
1201 GTFIVGSVEL LLMBE

!!AA_SEQUENCE 1.0
ID_CCR4_YEAST STANDARD; PRT; 837 AA.
AC P31384;
DT 01-JUL-1993 (Rel. 26, Created);
DT 01-JUL-1993 (Rel. 26, Last sequence update);
DT 15-JUN-2002 (Rel. 41, Last annotation update);
DE Glucose-repressible alcohol dehydrogenase transcriptional effector
DE (Carbon catabolite repressor protein 4).
GN CCR4 OR YAL021C OR FUN27.
OC Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=93093455; PubMed=1459446;
RA Malvar T., Biron R.W., Kaback D.B., Denis C.L.;
RT "The CCR4 protein from Saccharomyces cerevisiae contains a
RT leucine-rich repeat region which is required for its control of ADH2
RT gene expression.";
RL Genetics 132:951-962(1992).
RN [2];
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RX MEDLINE=93209532; PubMed=8458570;
RA Ouelllette B.F.F., Clark M.W., Keng T., Storms R.K., Zhong W.W.,
RA Zeng B., Fortin N., Delaney S., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I from Saccharomyces cerevisiae: analysis
RT of a 32 kb region between the LTR1 and SPO7 genes.";
RL Genome 36:32-42(1993).
RN [3];
RP SEQUENCE FROM N.A.
RX MEDLINE=94193531; PubMed=8144453;
RA Barton A.B., Kaback D.B.;
RT "Molecular cloning of chromosome I DNA from Saccharomyces cerevisiae:
RT analysis of the genes in the FUN38-MAK16-SPO7 region.";
RL J. Bacteriol. 176:1872-1880(1994).
CC -!- FUNCTION: CONTROL OF ADH2 GENE EXPRESSION. IT IS REQUIRED FOR THE
CC EXPRESSION OF GENES INVOLVED IN NONFERMENTATIVE GROWTH AND IT
CC MEDIATES OR IS REQUIRED FOR THE ACTION OF THE SPT6 & SPT10 GENES.
CC -!- MISCELLANEOUS: THE 169 CARBOXYL-TERMINAL RESIDUES ARE IMPORTANT
CC FOR CCR4 FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE CCR4/NOCTURIN FAMILY.
CC -!- SIMILARITY: TO YEAST CYC8/SGN6.
CC -!- SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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> O <
O | O IntelliGenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq448-wpat" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.
Selected sequence key from "new.key":
seq448 (AA) ID seq448 AA preliminary pattern
followed by
1 w o r e o r l o r a o r r o r s
2 y o r f o r e o r c o r n
2 d
2 p o r s o r t o r f o r l o r y o r c o r a
2 i t
2 k o r n o r q o r g o r r
2 l
2 w o r s o r t o r r o r c o r y o r k
2 l o r f o r v o r i o r h

Selected data banks and files:

Data bank : A-GeneSeq 35.2, all entries

-- Output Parameters --

Format Options:
Nucleic acid code matching Exact File Options:
Find non-matching hits only No Indirect file
Report key used Yes Sequence or key file
Note position of hit Yes List of hits
Display full annotations Yes Hit display
Sequence context 50 Name and annotations
Yes

-- Run Parameters --

Run mode Batch
Time to start comparison now
Notify at end of run No

No hits found.

-- Search Statistics --

Times: CPU Total Elapsed
00:01:14.09 00:01:24.00

Number of sequences searched: 170751
Number of sequence hits: 0
Number of separate matches: 0
Number of sequence hits saved: 0
```

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2003, 17:08:56 ; Search time 14 Seconds
(without alignments)
68.667 Million cell updates/sec

Title: US-09-932-613-448

Perfect score: 25

Sequence: 1 XXDXLTXLXX 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	76.0	80	2 H75472	hypothetical prote
2	19	76.0	115	2 T36886	hypothetical prote
3	19	76.0	123	2 D84383	hypothetical prote
4	19	76.0	125	2 AC1614	hypothetical prote
5	19	76.0	129	2 A86162	protein P1003.7 (i
6	19	76.0	130	2 E85042	hypothetical prote
7	19	76.0	144	2 PC4118	transcription init
8	19	76.0	146	2 A35720	hypothetical 16.1K
9	19	76.0	148	2 F86899	hypothetical prote
10	19	76.0	174	2 JC1382	hypothetical 20K p
11	19	76.0	185	2 F84182	hypothetical prote
12	19	76.0	196	2 AC0288	probable membrane
13	19	76.0	201	2 AI2631	hypothetical prote
14	19	76.0	206	2 JC1235	transcription fact
15	19	76.0	233	1 F89178	conserved hypothet
16	19	76.0	236	2 S30106	adenylate iscpente
17	19	76.0	248	2 AC0630	response regulator
18	19	76.0	253	2 E75570	gidB protein - Dei
19	19	76.0	254	2 S75676	probable phosphos
20	19	76.0	254	2 A82516	hypothetical prote
21	19	76.0	261	2 A50399	rhodanese-like pro
22	19	76.0	261	2 D31032	enhanced serine se
23	19	76.0	261	2 AFC823	SesB protein (Impo
24	19	76.0	261	2 B95273	hypothetical prote
25	19	76.0	264	2 A71708	acyl-l-acyl-carrier
26	19	76.0	269	2 H85896	enhanced serine se
27	19	76.0	277	2 G75505	hypothetical prote
28	19	76.0	278	2 T08647	hypothetical prote
29	19	76.0	297	2 F84378	sodium-dependent p

30 19 76.0 298 2 F87499 conserved hypothet
31 19 76.0 302 2 G81158 conserved hypothet
32 19 76.0 313 2 T23189 hypothetrical prote
33 19 76.0 313 2 H97585 carbohydrate kinas
34 19 76.0 313 2 A12806 carbohydrate kinas
35 19 76.0 314 2 S31868 glucocorticoid rec
36 19 76.0 319 2 T25666 hypothetrical prote
37 19 76.0 320 2 AF2714 conserved hypothet
38 19 76.0 324 2 A82357 cystathionine beta
39 19 76.0 328 2 A82087 phosphoserine phos
40 19 76.0 332 2 S15579 ipad protein - Shi
41 19 76.0 339 2 A83274 UDP-N-acetylpyruvo
42 19 76.0 343 2 AF3292 chemotaxis mota pr
43 19 76.0 352 2 T35891 hypothetrical prote
44 19 76.0 352 2 C97496 hypothetrical prote
45 19 76.0 353 2 T45280 probable ABC trans

ALIGNMENTS

RESULT 1

H75472 hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C;Accession: H75472

R;White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: H75472

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-80 <WHI>

A;Cross-references: GB:AE001935; GB:AE000513; NID:G6458517; PIDN:AAF10390.1; PID:G6458

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0803

A;Map position: 1

Query Match 76.0%; Score 19; DB 2; Length 80;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8

Db 43 DALTSL 48

RESULT 2

T36886 hypothetical protein SC151.23c - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T36886

R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, August 1999

A;Reference number: Z21617

A;Accession: T36886

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-115 <MUR>

A;Cross-references: EMBL:AL109848; PIDN:CA852847.1; GSPDB:GN00070; SCOEDB:SC151.23c

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SC151.23c

Query Match 76.0%; Score 19; DB 2; Length 115;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
DB 82 DALTAL 87

RESULT 3

D84383
hypothetical protein Vng2324h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84383
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
A:Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omar, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: D84383
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <STO>
A:Cross-references: GB:AE004437; NID:gi0581736; PIDN:AAG20432.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG2324H

Query Match 76.0%; Score 19; DB 2; Length 123;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
DB 108 DALTTL 113

RESULT 4

AC1614
hypothetical protein lin1452 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1614
R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1614
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96683.1; PID:gi6413925; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin1452

Query Match 76.0%; Score 19; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
DB 62 DSU TTL 67

RESULT 5

A86162
protein F1003.7 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A86162
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Aloni
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, I.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maici, R.; Marzila
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <STO>
A:Cross-references: GB:AE005172; NID:g4587567; PIDN:AAD25798.1; GSPDB:GN00141
C:Genetics:
A:Gene: F1003.7
A:Map position: 1

Query Match 76.0%; Score 19; DB 2; Length 129;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
DB 27 DLTSL 32

RESULT 6

B65042
hypothetical protein b2635 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: B65042
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B65042
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-130 <BLAT>
A:Cross-references: GB:AE000349; GB:U00096; NID:G2367143; PIDN:AAC75683.1; PID:G23671.
A:Experimental source: strain K-12, substrain MG1655

Query Match 76.0%; Score 19; DB 2; Length 130;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
DB 75 DSLTAL 80

RESULT 7

PC4118
transcription initiation factor sigma homolog - Pyrococcus sp. (fragment)
C:Species: Pyrococcus sp.
C:Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Jul-1997
C:Accession: PC4118
R:Ashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A:Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.
A:Reference number: JC4514; MUID:96105215; PMID:8529878
A:Accession: PC4118
A:Molecule type: DNA
A:Residues: 1-144 <RAS>
A:Cross-references: DDBJ:D50018
A:Note: the authors translated the codon AGC for residue 27 as Arg
C:Keywords: DNA binding; sigma factor; transcription initiation

Gene 121, 103-110, 1992
 A;Title: Protein-coding introns from the 23S rRNA-encoding gene form stable circles in
 A;Reference number: JCI382; MUID:93051344; PMID:1427083
 A;Accession: JCI382
 A;Molecule type: DNA
 A;Residues: 1-174 <DAL>
 A;Cross-references: GB:M86622
 C;Genetics:
 A;Start codon: GTG

Query Match 76.0%; Score 19; DB 2; Length 144;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
 | | | |
 Db 118 DALTAL 123

RESULT 8
 A35720
 hypothetical 16.1K protein (phnQ 3' region) - Escherichia coli
 N;Alternate names: hypothetical protein 146
 C;Species: Escherichia coli
 C;Date: 05-Oct-1990 #sequence_revision 19-Mar-1993 #text_change 04-Mar-2000
 C;Accession: A35720
 R;Chen, C.M.; Ye, Q.Z.; Zhu, Z.; Wanner, B.L.; Walsh, C.T.
 J. Biol. Chem. 265, 4461-4471, 1990
 A;Title: Molecular biology of carbon-phosphorus bond cleavage. Cloning and sequencing of
 A;Reference number: A35718; MUID:90170953; PMID:2155230
 A;Accession: A35720
 A;Molecule type: DNA
 A;Residues: 1-146 <CHS>
 A;Cross-references: GB:J05260; NID:gl47192; PIDN:AAA24342.1; PID:gw455181
 C;Genetics:
 A;Start codon: GTG
 C;Superfamily: Escherichia coli hypothetical 16.1K protein (phnQ 3' region)

Query Match 76.0%; Score 19; DB 2; Length 146;
 Best Local Similarity 66.7%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
 | | | |
 Db 61 DALTAL 66

RESULT 9
 F86899
 hypothetical protein ywId [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C;Accession: F86899
 R;Bolotin, A.; Winker, P.; Mauger, S.; Jaillon, O.; Maitame, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A;Reference number: A86625; MUID:21235186; PMID:1133747;
 A;Accession: F86899
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-148 <STO>
 A;Cross-references: GB:AB005176; PID:gl2725263; PIDN:AAK06296.1; GSPDB:GN00146
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: ywId

Query Match 76.0%; Score 19; DB 2; Length 148;
 Best Local Similarity 66.7%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
 | | | |
 Db 8 DLTAL 13

RESULT 10
 JCI382
 hypothetical 20K protein (rRNA intron) - Pyrobaculum organotrophum
 C;Species: Pyrobaculum organotrophum
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
 C;Accession: JCI382
 R;Dalgaard, J.Z.; Garrett, R.A.

Gene 121, 103-110, 1992
 A;Title: Protein-coding introns from the 23S rRNA-encoding gene form stable circles in
 A;Reference number: JCI382; MUID:93051344; PMID:1427083
 A;Accession: JCI382
 A;Molecule type: DNA
 A;Residues: 1-174 <DAL>
 A;Cross-references: GB:M86622
 C;Genetics:
 A;Start codon: GTG

Query Match 76.0%; Score 19; DB 2; Length 174;
 Best Local Similarity 66.7%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
 | | | |
 Db 120 DALTAL 125

RESULT 11
 F84182
 hypothetical protein Vng0219h [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: F84182
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
 ; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jar
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: F84182
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-185 <STO>
 A;Cross-references: GB:AE004437; NID:gl0579866; PIDN:AAG18826.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: VNG0219H

Query Match 76.0%; Score 19; DB 2; Length 185;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
 | | | |
 Db 145 DALTAL 150

RESULT 12
 AC0288
 probable membrane protein YPO2362 [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C;Accession: AC0288
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
 deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
 ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AC0288
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-196 <KUR>
 A;Cross-references: GB:AL590842; PIDN:CAC91167.1; PID:gl5980359; GSPDB:GN00175
 C;Genetics:
 A;Gene: YPO2362

Query Match 76.0%; Score 19; DB 2; Length 196;
 Best Local Similarity 66.7%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
Db 65 DLTAL 70

RESULT 13

A12631
hypothetical protein Atu0452 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: A12631
R:Wood, D.W.; Stutbal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillat, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: A12631
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <XUR>
A:Cross-references: GB:AE008688; PIDN:AAL41471.1; PID:gi7738796; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0452
A:Map position: circular chromosome

Query Match 76.0%; Score 19; DB 2; Length 201;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
Db 107 DALTSL 112

RESULT 14

JC1235
transcription factor BTF3a - human
N:Contains: transcription factor BTF3b
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C:Accession: JC1235; JC1236; S09160; S09161; S34664
R:Kanno, M.; Chalut, C.; Egly, J.M.
Gene 117, 219-228, 1992
A:Title: Genomic structure of the putative BTF3 transcription factor.
A:Reference number: JC1235; PMID:92347696; PMID:1386332
A:Accession: JC1235
A:Molecule type: DNA
A:Residues: 1-206 <KAN>
A:Cross-references: GB:M90352; GB:M90357
A:Note: the authors translated the codon GAG for residue 41 as Gln
A:Accession: JC1236
A:Molecule type: DNA
A:Residues: 45-206 <KA2>
R:Zheng, X.M.; Black, D.; Chambon, P.; Egly, J.M.
Nature 344, 556-559, 1990
A:Title: Sequencing and expression of complementary DNA for the general transcription fa
A:Reference number: S09160; PMID:9026080; PMID:2320128
A:Accession: S09160
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-40, 'Q', 42-206 <ZH2>
A:Cross-references: GB:X53280; NID:G29504; PIDN:CAA37375.1; PID:G29505
A:Note: part of this sequence was confirmed by amino acid sequencing
A:Accession: S09161
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 45-206 <ZH3>
A:Cross-references: GB:X53281; NID:G29506; PIDN:CAA37376.1; PID:G29507

A:Note: part of this sequence was confirmed by amino acid sequencing
R:Leffers, H.; Honore, B.; Madsen, A.; Nielsen, M.S.; Anderson, A.H.; Cells, J.E.
submitted to the EMBL Data Library, July 1993
A:Description: cDNA expression and human 2D-gel data bases: towards integrating prote
A:Reference number: S34664
A:Accession: S34664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 45-206 <LEF>
A:Cross-references: EMBL:X74070; NID:G395086; PIDN:CAA52200.1; PID:G395087
C:Genetics:
A:Gene: GDB:BTF3
A:Cross-references: GDB:135165
A:Map position: 9q13-9q13
A:Introns: 44/3; 67/3; 105/3; 173/1; 191/1
C:Superfamily: transcription factor BTF3
C:Keywords: alternative splicing; transcription factor

Query Match 76.0%; Score 19; DB 2; Length 206;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
Db 157 DSLTSL 162

RESULT 15

F69178
conserved hypothetical protein MTH593 - Methanobacterium thermoautotrophicum (strain
C:Species: Methanobacterium thermoautotrophicum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: F69178
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan,
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A:Reference number: A69000; PMID:98037514; PMID:93711463
A:Accession: F69178
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <MTH>
A:Cross-references: GB:AB000841; GB:AB000666; NID:G2621665; PIDN:AA885099.1; PID:G262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH593
C:Superfamily: conserved hypothetical protein MTH593

Query Match 76.0%; Score 19; DB 1; Length 233;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXLTXL 8
| | | |
Db 141 DSLTTL 146

Search completed: May 24, 2003, 17:13:15
Job time : 17 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 17:01:16 ; Search time 7 Seconds
(without alignments)
59.252 Million cell updates/sec

Title: US-09-932-613-448
Perfect score: 25
Sequence: 1 XDXLTXLXX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	76.0	78	1 YPJX_ECOLI	P52134 escherichia
2	19	76.0	204	1 BTF3_MOUSE	Q64152 mus musculus
3	19	76.0	206	1 BTF3_MOUSE	P20290 homo sapien
4	19	76.0	214	1 BTF3_MOUSE	Q13832 homo sapien
5	19	76.0	236	1 IPT1_AGRVI	Q04590 agrobacteri
6	19	76.0	253	1 AABA_BACNO	P39906 bacteroides
7	19	76.0	253	1 GIDB_DEIRA	Q9rv66 deinococcus
8	19	76.0	258	1 SREB_ECOLI	P31143 escherichia
9	19	76.0	264	1 LPXA_RICPR	Q32653 rickettsia
10	19	76.0	297	1 Y630_METJA	Q58047 methanococc
11	19	76.0	314	1 GCR_SHEEP	P35547 ovis aries
12	19	76.0	332	1 IPAD_SHIDY	Q03947 shigella dy
13	19	76.0	338	1 YABT_BACSU	P37562 bacillus su
14	19	76.0	339	1 RAS1_USTMA	Q99133 ustilago ma
15	19	76.0	362	1 ERD1_YEAST	P26151 saccharomyc
16	19	76.0	382	1 NUSA_BACHD	Q9x474 bacillus ha
17	19	76.0	385	1 DIAC_HUMAN	Q01459 homo sapien
18	19	76.0	385	1 HISZ_HABIN	P71344 haemophilus
19	19	76.0	392	1 HISZ_LISIN	Q92682 listeria in
20	19	76.0	393	1 HISZ_LISMO	Q9y9t9 listeria mo
21	19	76.0	403	1 V271_AQUAE	Q66628 aquifex aeo
22	19	76.0	409	1 YH65_MYCTU	Q50697 mycobacteri
23	19	76.0	421	1 FAJ1_HUMAN	Q92949 homo sapien
24	19	76.0	421	1 FAJ1_MOUSE	Q16660 mus musculu
25	19	76.0	421	1 FXJ1_RAT	Q63247 rattus norv
26	19	76.0	435	1 GLSF_HORVU	Q08258 hordeum vul
27	19	76.0	449	1 DHE2_CLOSD	P24295 clostridium
28	19	76.0	457	1 MURF_BACSU	P96613 bacillus su
29	19	76.0	477	1 PAC2_XENLA	Q9dd39 xenopus lae
30	19	76.0	485	1 OC90_MOUSE	Q92013 mus musculu
31	19	76.0	510	1 YH43_YEAST	Q03218 saccharomyc
32	19	76.0	530	1 LMT_RHILO	Q98b36 rhizobium l
33	19	76.0	582	1 SHO2_HUMAN	Q9aug13 homo sapien

34	19	76.0	582	1 SHO2_MOUSE	O88520 mus musculu
35	19	76.0	667	1 ENV_GALV	P21415 gibbon ape
36	19	76.0	758	1 PURL_CORAM	Q9rtw9 corynebacte
37	19	76.0	795	1 GCR_RAT	P06536 rattus norv
38	19	76.0	1012	1 POLG_IBDVO	P27276 avian infec
39	19	76.0	1115	1 YAA4_SCHPO	Q09798 schizosacch
40	19	76.0	1233	1 NMES_HUMAN	Q14957 homo sapien
41	19	76.0	1237	1 NMES_RAT	Q00961 rattus norv
42	19	76.0	1239	1 NMES_MOUSE	Q01098 mus musculu
43	19	76.0	1380	1 CYAA_LEIDO	Q27675 leishmania
44	19	76.0	1517	1 GLSF_SPIOL	Q43155 spinacia ol
45	18	72.0	96	1 GATC_DEIRA	Q9ruv6 deinococcus

ALIGNMENTS

RESULT 1
YPJK_ECOLI
ID YPJX_ECOLI STANDARD; PRT; 78 AA.
AC P52134; AC
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ypjK precursor.
GN YPJX OR B2635.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -!- SIMILARITY: STRONG, TO E.COLI YKFL.
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CC -----
CC EMBL; U36840; AAA79804.1; ALT FRAME.
CC EMBL; AB000349; AAC75683.1; ALT INIT.
CC EcoGene; EGI4379; YpjK.
CC KW Hypothetical protein; Signal; Complete proteome.
CC SIGNAL 1 45 POTENTIAL.
CC CHAIN 46 78 HYPOTHETICAL PROTEIN YPJX.
CC SEQUENCE 78 AA; 7703 MW; 9DE01A5E14D2E6A CRC64;
Query Match 76.0%; Score 19; DB 1; Length 78;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DLTXL 8
DB 23 DLTAL 28
RESULT 2
BTF3_MOUSE
ID BTF3_MOUSE STANDARD; PRT; 204 AA.
AC Q64152; Q64153;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

```

15-JUN-2002 (Rel. 41, Last annotation update)
DE Transcription factor BTF3 (RNA polymerase B transcription factor 3).
GN BTF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 43-65 AND 104-158 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95384207; PubMed=7655515;
RA Deng J.M., Behringer R.R.;
RT "An insertional mutation in the Btf3 transcription factor gene leads
RL to an early postimplantation lethality in mice."
RN Transgenic Res. 4:264-269(1995).
[2]
RP SEQUENCE OF 1-162 AND 43-204 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RA Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
RA Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
RA Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
RA Theising B., Wylie I., Lennon G., Soares B., Wilson R., Waterston R.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN RECONSTRUCTION FROM ESTS, AND CONCEPTUAL TRANSLATION.
RP Wanders A.;
RL Unpublished observations (DEC-1997).
CC -!- FUNCTION: GENERAL TRANSCRIPTION FACTOR. BTF3 CAN FORM A STABLE
CC COMPLEX WITH RNA POLYMERASE II. REQUIRED FOR THE INITIATION OF
CC TRANSCRIPTION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE BTF3 TRANSCRIPTION FACTORS FAMILY.
CC -!- CAUTION: THIS IS A RECONSTRUCTION FROM A DNA FRAGMENT AND THREE
CC DIFFERENT ESTS, NONE OF WHICH CODING FOR THE COMPLETE BTF3A. IN
CC ONE OF THEM (AA015403) FRAMESHIFTS HAVE BEEN INTRODUCED AT
CC POSITIONS 22, 26 AND 36; AS THE OTHER ESTS CODE FOR BTF3B
CC (STARTING AT POSITION 43) ONLY, THE SEQUENCE OF 1-42 MAY BE
CC UNSURE.
-----
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-----
DR EMBL; S79538; -; NOT_ANNOTATED_CDS.
DR EMBL; S79537; -; NOT_ANNOTATED_CDS.
DR EMBL; AA220754; -; NOT_ANNOTATED_CDS.
DR EMBL; AA220626; -; NOT_ANNOTATED_CDS.
DR EMBL; AA015403; -; NOT_ANNOTATED_CDS.
DR MGD; MGI:1202875; Btf3.
DR InterPro; IPR002715; NAC.
DR Pfam; PF01849; NAC; 1.
KW Transcription regulation; Nuclear protein; Alternative splicing.
FT CHAIN 1 204
FT BTF3A (BY SIMILARITY).
FT CHAIN 43 204
FT BTF3B (BY SIMILARITY).
FT CONFLICT 47 47 I -> V (IN REF. 1).
FT CONFLICT 55 55 K -> E (IN REF. 2; AA015403).
FT CONFLICT 55 55 K -> R (IN REF. 1).
FT CONFLICT 109 109 N -> S (IN REF. 1).
FT CONFLICT 149 150 LN -> RH (IN REF. 2; AA015403).
SQ SEQUENCE 204 AA; 21999 MW; 78318EC1E01C9523 CRC64;
Query Match 76.0%; Score 19; DB 1; Length 204;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DLTXTL 8
DB 155 DSLTSL 160

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RESULT 3
BTF3_HUMAN
ID BTF3_HUMAN STANDARD; PRT; 206 AA.
AC P20290; Q13893;
DC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Transcription factor BTF3 (RNA polymerase B transcription factor 3).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90206080; PubMed=2320128;
RA Zheng X.M., Black D., Chambon P., Egly J.-M.;
RT "Sequencing and expression of complementary DNA for the general
RL transcription factor BTF3."
RN Nature 344:556-559(1990).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=92347696; PubMed=1386332;
RA Kanno M., Chalut C., Egly J.-M.;
RT "Genomic structure of the putative BTF3 transcription factor.";
RL Gene 117:219-228(1992).
CC -!- FUNCTION: GENERAL TRANSCRIPTION FACTOR. BTF3 CAN FORM A STABLE
CC COMPLEX WITH RNA POLYMERASE II. REQUIRED FOR THE INITIATION OF
CC TRANSCRIPTION.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; BTF3A (SHOWN HERE) AND BTF3B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. BTF3B IS TRANSCRIPTIONALLY
CC INACTIVE DESPITE ITS ABILITY TO BIND RNAP II.
CC -!- SIMILARITY: BELONGS TO THE BTF3 TRANSCRIPTION FACTORS FAMILY.
-----
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-----
DR EMBL; X53280; CAA37375.1; -.
DR EMBL; M90357; AAA58398.1; -.
DR PIR; S09160; S09160.
DR PIR; S09161; S09161.
DR Genew; HGNC:1125; BTF3.
DR MIM; 602542; -.
DR InterPro; IPR002715; NAC.
DR Pfam; PF01849; NAC; 1.
KW Transcription regulation; Nuclear protein; Alternative splicing.
FT CHAIN 1 206
FT BTF3A.
FT CHAIN 45 206
FT BTF3B.
FT CONFLICT 41 41 O -> E (IN REF. 2).
FT CONFLICT 68 105 MISSING (IN REF. 2).
FT CONFLICT 192 196 DLVEN -> GG (IN REF. 2).
FT CONFLICT 198 198 D -> Q (IN REF. 2).
SQ SEQUENCE 206 AA; 22168 MW; 9653AC480EAF64C6 CRC64;
Query Match 76.0%; Score 19; DB 1; Length 206;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DLTXTL 8
DB 157 DSLTSL 162

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RESULT 4

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BT33_HUMAN
ID   BT33_HUMAN          STANDARD;          PRT;          214 AA.
AC   Q13892;
DT   01-NOV-1997 (Rel. 35, Created)
DI   01-NOV-1997 (Rel. 35, Last sequence update)
DI   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Transcription factor BTF3 homolog 3.
GN   BTF3L3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leukocyte;
RX   MEDLINE=2347696; PubMed=1386332;
RA   Kanno M., Chalut C., Egly J.-M.;
RT   "Genomic structure of the putative BTF3 transcription factor.";
RL   Gene 117:219-228(1992).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE BTF3 TRANSCRIPTION FACTORS FAMILY.
CC   -----
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CC   -----
CC   EMBL; M90356; AAA58401.1; -.
CC   Genew; HGNC:1128; BTF3L3.
CC   MIM; 603739; -.
CC   InterPro; IPR002715; NAC.
CC   Pfam; PF01849; NAC; 1.
CC   Transcription regulation; Nuclear protein.
KW   TRANSCRIPTION REGULATION; NUCLEAR PROTEIN.
SQ   SEQUENCE 214 AA; 23373 MW; 1CCFDDA009ADE32 CRC64;
Query Match 76.0%; Score 19; DB 1; Length 214;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DLTXL 8
DB 143 DLTSL 148
RESULT 5
ID   IPT1_AGRVI          STANDARD;          PRT;          236 AA.
AC   Q04590;
DT   01-NOV-1995 (Rel. 32, Created)
DI   01-NOV-1995 (Rel. 32, Last sequence update)
DI   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Isopentenyl transferase (dimethylallyl transferase) (EC 2.5.1.-).
GN   IPT.
OS   Agrobacterium vitis (Rhizobium vitis).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=373;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S4;
RX   MEDLINE=93101133; PubMed=1465104;
RA   Canaday J., Gerard J.-C., Crouzet P., Otten L.;
RT   "Organization and functional analysis of three T-DNAs from the
RT   vitopine Ti plasmid pTiS4.";
RL   Mol. Gen. Genet. 235:292-303(1992).
CC   -!- FUNCTION: THIS IS ONE OF THE ENZYMES INVOLVED IN THE BIOSYNTHESIS
CC   OF THE CYTOKININS PHYTOHORMONES AND IN SHOOT FORMATION.
CC   -----
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CC   -----
CC   EMBL; N91610; AAA98150.1; -.
CC   InterPro; IPR002648; IPT.
CC   Pfam; PF01745; IPT; 1.
CC   ProDom; PD005388; IPT; 1.
CC   Transferrase; plasmid; Cytokinin biosynthesis; T-DNA;
CC   Crown gall tumor.
CC   SEQUENCE 236 AA; 25840 MW; 31ECC9A17F2D1DF CRC64;
Query Match 76.0%; Score 19; DB 1; Length 236;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DLTXL 8
DB 190 DLTSL 195
RESULT 6
ID   AABA_BACNO          STANDARD;          PRT;          253 AA.
AC   P39906;
DT   01-FEB-1995 (Rel. 31, Created)
DI   01-FEB-1995 (Rel. 31, Last sequence update)
DI   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Amino-acid binding protein aabA precursor.
GN   AABA.
OS   Bacteroides nodosus (Dichelobacter nodosus).
OC   Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC   Dichelobacter.
OX   NCBI_TaxID=870;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A198;
RX   MEDLINE=95291444; PubMed=7539688;
RA   Billington S.J., Jost B.H., Rood J.I.;
RT   "A gene region in Dichelobacter nodosus encoding a lipopolysaccharide
RT   epitope.";
RL   Microbiology 141:945-957(1995).
CC   -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC   -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC   PROTEIN FAMILY 3.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; U06471; AAC43388.1; -.
CC   InterPro; IPR001311; SBP/glu receptor.
CC   InterPro; IPR001638; SBP_bac_3.
CC   Pfam; PF00497; SBP_bac_3; 1.
CC   SMART; SM00062; PBB; 1.
CC   PROSITE; PS01039; SBP_BACTERIAL_3; 1.
CC   Transferrase; Amino-acid transport; Periplasmic; Signal.
CC   SIGNAL 1 23 POTENTIAL.
CC   FT CHAIN 24 253 AMINO-ACID BINDING PROTEIN AABA.
CC   SEQUENCE 253 AA; 28213 MW; 82F291F90D7D5E29 CRC64;
Query Match 76.0%; Score 19; DB 1; Length 253;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DLTXL 8

```

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Db 78 DTOTAL 83
|||||
RESULT 7
ID GIDB DEIRA STANDARD; PRT; 253 AA.
AC Q9RV56;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methyltransferase gidb (EC 2.1.1.-) (Glucose inhibited division
protein B)
DE protein B)
GN GIDB OR DR0014.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
CC -!- FUNCTION: Probable S-adenosyl-L-methionine dependent
CC methyltransferase specific for a sterol and/or lipid substrate (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE GIDB FAMILY.
CC -----
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CC -----
DR ENBL; AEO01865; AAF09607.1; -
DR TIGR; DR0014; -
DR InterPro; IPR003692; GidB.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF02527; GidB; 1.
DR ProDom; PD004441; GidB; 1.
DR TIGRFAMs; TIGR00139; gidb; 1.
KW Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 253 AA; 27522 MW; 63308D03D59776D0 CRC64;

Query Match 76.0%; Score 19; DB 1; Length 253;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDLTXL 8
| | | |
Db 64 DSLTTL 69

RESULT 8
SSEB_ECOLI STANDARD; PRT; 258 AA.
ID SSEB_ECOLI
AC P31143; P76579;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein sseB.
GN SSEB OR B2522.

Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3133-2;
RX MEDLINE=95073976; PubMed=7982894;
RA Hama H., Kayahara T., Ogawa M., Teuda M., Tsuchiya T.;
RT "Enhancement of serine-sensitivity by a gene encoding rhodanese-like
protein in Escherichia coli.";
RL J. Biochem. 115:1135-1140(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=9426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizubuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sanpei G., Satoh Y., Sivaundaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
K-12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -!- FUNCTION: MAY BE INVOLVED IN THE ENHANCEMENT OF SERINE-
CC SENSITIVITY.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to
CC frameshifts.
CC -----
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CC -----
DR ENBL; D10456; BAA01383.1; ALT_FRAME.
DR ENBL; AE000339; BAC75575.1; ALT_INIT.
DR ENBL; D90882; BAA16412.1; ALT_INIT.
DR PIR; JC2271; JC2271.
DR EcoGene; EG11601; sseB.
KW Complete proteome.
SQ SEQUENCE 258 AA; 28642 MW; EEFCDGD2D76D195A CRC64;

Query Match 76.0%; Score 19; DB 1; Length 258;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDLTXL 8
| | | |
Db 156 DSLTTL 161

RESULT 9
LPXA_RICPR STANDARD; PRT; 264 AA.
ID LPXA_RICPR
AC Q9ZED5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

```

DE Acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase
 DE (EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase).
 GN LPXA OR P007.
 OS Rickettsia prowazekii.
 OS Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 ON NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99033499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria";
 RL Nature 396:133-140(1998).
 CC -!- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF LIPID A, A
 CC THE OUTER MEMBRANE OF THE CELL (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: (R)-3-hydroxytetradecanoyl-[acyl-carrier
 CC protein] + UDP-N-acetylglucosamine = [acyl-carrier protein] +
 CC UDP-3-O-(3-hydroxytetradecanoyl)-N-acetylglucosamine.
 CC -!- PATHWAY: Lipid A biosynthesis; first step.
 CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TRANSFERASE HEXAPEPTIDE REPEAT FAMILY.
 CC LPXA SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ235270; CAAL4480.1; -;
 DR HSSP; P10440; ILXA.
 DR InterPro; IPR001451; Hexapep_transf.
 DR Pfam; PF00132; hexapep; 8.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
 KW Transferase; Acyltransferase; Lipid A biosynthesis; Lipid synthesis;
 KW Repeat; Complete proteome.
 SQ SEQUENCE 264 AA; 28470 MW; 9FA749DC2B5BCE61 CRC64;

 Query Match 76.0%; Score 19; DB 1; Length 264;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 Qy 3 DXTLXL 8
 Db 209 DSLTAL 214

 RESULT 10
 Y630 METJA
 ID Y630 METJA STANDARD; PRT; 297 AA.
 AC Q58047;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0630.
 GN MJ0630.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Karlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glöckle A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii";
 RL Science 273:1058-1073(1996).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -----
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 CC -----
 CC EMBL; U67510; AAB98622.1; -;
 DR TIGR; MJ0630; -;
 DR InterPro; IPR001204; Phos_transp.
 DR Pfam; PF01384; PHO4; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 2 22 POTENTIAL.
 FT TRANSMEM 45 65 POTENTIAL.
 FT TRANSMEM 67 87 POTENTIAL.
 FT TRANSMEM 99 119 POTENTIAL.
 FT TRANSMEM 121 141 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 180 200 POTENTIAL.
 FT TRANSMEM 225 245 POTENTIAL.
 FT TRANSMEM 274 294 POTENTIAL.
 SQ SEQUENCE 297 AA; 33036 MW; 4AS1B12ADE68026C CRC64;

 Query Match 76.0%; Score 19; DB 1; Length 297;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 Qy 3 DLTXL 8
 Db 73 DALFAL 78

 RESULT 11
 GCR SHEEP
 ID GCR SHEEP STANDARD; PRT; 314 AA.
 AC P35547;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glucocorticoid receptor (GR) (Fragment).
 GN NR3C1 OR GR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92384893; PubMed=1515021;
 RA Yang K., Hammond G.L., Challis J.R.;
 RT "Characterization of an ovine glucocorticoid receptor cDNA and
 RT developmental changes in its mRNA levels in the fetal sheep
 RT hypothalamus, pituitary gland and adrenal";
 RL J. Mol. Endocrinol. 8:173-180(1992).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. BINDS TO THE
 CC GRE TARGET SITE.
 CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 CC NR3 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; X70407; CAA49851.1; -;
 DR EMBL; S44554; AAB23141.1; -;
 DR PIR; S31868; S31868.
 DR HSSP; P06536; IGDC.
 DR InterPro; IPR001409; G1crtcd_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00105; Zf-C4; 1.
 DR Pfam; PF02155; GCR; 1.
 DR ProDom; PD000039; Znf_C4steroid; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Steroid-binding.
 KW NON_TER 1 1
 FT DOMAIN <1 281 MODULATING.
 FT DNA_BIND 282 >314 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 282 >314 C4-TYPE.
 FT NON_TER 314 314
 SQ SEQUENCE 314 AA; 33562 MW; 5899DCB75B79CAD8 CRC64;
 Query Match 76.0%; Score 19; DB 1; Length 314;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DXLTXL 8
 DB 235 DSLTSL 240
 RESULT 12
 ID IPAD_SHIDY STANDARD; PRT; 332 AA.
 AC Q03947;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 37 kDa membrane antigen ipad.
 GN IPAD.
 OS Shigella dysenteriae.
 OG Plasmid invasion.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 OC Shigella.
 OX NCBI_TaxID=622;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CG097;
 RX MEDLINE=92114800; PubMed=1766387;
 RA Yao R., Palchaudhuri S.;
 RT "Nucleotide sequence of the ipaBCD structural genes of Shigella
 RL Mol. Microbiol. 5:2217-2221 (1991).
 CC -----
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 CC -----

DR EMBL; X60777; CAA43192.1; -;
 DR PIR; S15579; S15579.
 KW Antigen; Virulence; Plasmid.
 SQ SEQUENCE 332 AA; 36598 MW; 916FE4B394E9046 CRC64;
 Query Match 76.0%; Score 19; DB 1; Length 332;
 Best Local Similarity 66.7%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DXLTXL 8
 DB 197 DALTTL 202
 RESULT 13
 YAST_BACSU
 ID YAST_BACSU STANDARD; PRT; 338 AA.
 AC P37552; O31415;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable serine/threonine-protein kinase yast (BC 2.7.1.1.-).
 GN YAST.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96051385; PubMed=7584024;
 RA Ogasawara N., Nakai S., Yoshikawa H.;
 RT "Systematic sequencing of the 180 kilobase region of the Bacillus
 RT subtilis chromosome containing the replication origin";
 RL DNA Res. 1:1-14 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guilbert G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Kullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Tateuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosiato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler B., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis";
 RL Nature 390:249-256 (1997)
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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EMBL; D26185; BAA05301.1; ALT INIT.
 EMBL; Z99104; CAB11842.1; ALT_INIT.
 Sublist; BG10129; YabT.
 InterPro; IPR000719; Euk_kinase.
 InterPro; IPR002290; Ser_thr_kinase.
 Pfam; PF00069; kinase; 1.
 PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 PROSITE; PS00108; PROTEIN KINASE-ST; FALSE_NEG.
 PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 ATP-binding; Complete proteome.
 DOMAIN 28 286 PROTEIN KINASE.
 FT BIND 34 42 ATP (BY SIMILARITY).
 BINDING 55 55 ATP (BY SIMILARITY).
 ACT SITE 148 148 BY SIMILARITY.
 ACT SITE 148 148 BY SIMILARITY.
 SEQUENCE 338 AA; 37665 MW; 71896CE0A0A03470 CRC64;

Query Match 76.0%; Score 19; DB 1; Length 338;
 Best Local Similarity 66.7%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDLTXL 8
 |||||
 Db 4 DALTSLS 9

RESULT 14

RAS1_USTMA
 ID RAS1_USTMA STANDARD; PRT; 339 AA.
 AC Q99133;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA repair protein RAD51.
 DE RAD51.
 OS Ustilago maydis (Smut fungus).
 CC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 CC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=5270;
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE=97223207; PubMed=9071580;
 RA Ferguson D.O., Rice M.C., Rendi M.H., Kotani H., Kmiec E.B.,
 RA Holloman W.K.;
 RT Interaction between Ustilago maydis REC2 and RAD51 genes in DNA
 RT repair and mitotic recombination.";

Genetics 145:243-251(1997).
 CC -!- FUNCTION: REQUIRED BOTH FOR RECOMBINATION AND FOR THE REPAIR OF
 CC DNA DAMAGE CAUSED BY X-RAYS (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY. RAD51 SUBFAMILY.
 CC
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EMBL; U62484; AAC61878.1; -
 DR HSP; Q06609; 1822.
 DR InterPro; IPR003583; HHH_1.
 DR InterPro; IPR000445; HHH.
 DR InterPro; IPR001553; RecA.
 Pfam; PF00633; HHH_1.
 DR ProDom; PD000229; RecA; 1.
 DR SMART; SM00278; HHH1; 1.

DR PROSITE; PS00162; RECA_2; 1.
 DR PROSITE; PS00163; RECA_3; 1.
 KW DNA damage; DNA repair; ATP-binding; DNA recombination.
 FT NP BIND 127 134 ATP (POTENTIAL).
 SQ SEQUENCE 339 AA; 36396 MW; D0E3676272FD0254 CRC64;

Query Match 76.0%; Score 19; DB 1; Length 339;
 Best Local Similarity 66.7%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDLTXL 8
 |||||
 Db 222 DSLTSL 227

RESULT 15

ERD1_YEAST
 ID ERD1_YEAST STANDARD; PRT; 362 AA.
 AC P16151;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ERD1 protein.
 GN ERD1 OR YDR141C OR D9461.4.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE=90183957; PubMed=2178921;
 RA Hardwick K., Lewis M., Semenza J., Dean N., Pelham H.;
 RT "ERD1, a yeast gene required for the retention of luminal endoplasmic
 RT reticulum proteins, affects glycoprotein processing in the Golgi
 RT apparatus.";
 RN EXBO J. 9:623-630(1990).
 RN [2]

PP SEQUENCE FROM N.A.
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
 RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
 RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
 RA Winant A., Yelton M., Botstein D., Davis R.W.;
 RL Nantant A., Yelton M., Botstein D., Davis R.W.;
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: REQUIRED FOR THE RETENTION OF LUMINAL ENDOPLASMIC
 CC RETICULUM PROTEINS, AFFECTS GLYCOPROTEIN PROCESSING IN THE
 CC GOLGI APPARATUS.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC
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 CC or send an email to license@isb-sib.ch).

EMBL; U33007; AAB64888.1; -
 DR EMBL; X51949; CAA36211.1; -
 DR FIR; S22841; S22841.
 DR SGD; S0002822; ERD1.
 DR InterPro; IPR004342; EXS_Cterm.
 DR Pfam; PF03124; EXS_1.
 DR Endoplasmic reticulum; Transmembrane; Protein transport.
 KW TRANSMEM 25 45 POTENTIAL.
 FT TRANSMEM 85 105 POTENTIAL.
 FT TRANSMEM 110 130 POTENTIAL.
 FT CONFLICT 168 168 G -> A (IN REF. 1).
 SQ SEQUENCE 362 AA; 43216 MW; 67925E8489410044 CRC64;

Query Match 76.0%; Score 19; DB 1; Length 362;
 Best Local Similarity 66.7%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8

Db 276 DSLTSL 281

Search completed: May 24, 2003, 17:11:42

Job time : 8 secs

GenCore version 5.1.4.p5_4578
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CM protein - protein search, using sw model

Run on: May 24, 2003, 17:06:21 ; Search time 25 Seconds
(without alignments)
82.419 Million cell updates/sec

Title: US-09-932-613-448
Perfect score: 25
Sequence: 1 XDXLTXLXX 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_xvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	76.0	70	Q8V6S0	Q8V6S0 halovirus h
2	19	76.0	76	Q94ML6	Q94ML6 bacterioph
3	19	76.0	80	Q9RW66	Q9RW66 deinococcus
4	19	76.0	101	Q9TTA7	Q9TTA7 macropus fu
5	19	76.0	115	Q9S217	Q9S217 streptomyce
6	19	76.0	118	Q8U346	Q8U346 pyrococcus
7	19	76.0	123	Q9HMY9	Q9HMY9 halobacteri
8	19	76.0	125	Q92BU2	Q92BU2 listeria in
9	19	76.0	129	Q9SA59	Q9SA59 arabidopsis
10	19	76.0	146	Q47480	Q47480 escherichia
11	19	76.0	148	Q9CDM1	Q9CDM1 lactococcus
12	19	76.0	157	Q8R6Q3	Q8R6Q3 thermoanaer
13	19	76.0	158	Q96K17	Q96K17 homo sapien
14	19	76.0	158	Q9CQR7	Q9CQR7 mus musculu
15	19	76.0	165	Q8VNT5	Q8VNT5 enterobacte
16	19	76.0	169	Q98B49	Q98B49 rhizobium 1

17	19	76.0	174	11	Q9CS78	Q9CS78 mus musculu
18	19	76.0	185	17	Q9HS10	Q9HS10 halobacteri
19	19	76.0	186	16	Q8X1K6	Q8X1K6 clostridium
20	19	76.0	187	2	Q9RNA7	Q9RNA7 microcystis
21	19	76.0	196	16	Q8Z224	Q8Z224 yersinia pe
22	19	76.0	201	16	Q8U148	Q8U148 agrobacteri
23	19	76.0	208	16	Q981G0	Q981G0 rhizobium 1
24	19	76.0	222	10	Q9XEL9	Q9XEL9 elaeis guin
25	19	76.0	229	16	Q9CLF5	Q9CLF5 pasteurella
26	19	76.0	233	17	Q26693	Q26693 methanobact
27	19	76.0	236	5	Q9NCP0	Q9NCP0 giardia lam
28	19	76.0	236	10	Q9LUM9	Q9LUM9 arabidopsis
29	19	76.0	242	11	Q9D8H9	Q9D8H9 mus musculu
30	19	76.0	248	2	Q85302	Q85302 salmonella
31	19	76.0	248	16	Q8ZQ53	Q8ZQ53 salmonella
32	19	76.0	248	16	Q8Z7Q7	Q8Z7Q7 salmonella
33	19	76.0	252	2	Q44226	Q44226 anabaena sp
34	19	76.0	252	2	Q05134	Q05134 pseudomonas
35	19	76.0	252	4	Q9B073	Q9B073 homo sapien
36	19	76.0	254	16	P74150	P74150 synchocyst
37	19	76.0	254	16	Q8YK18	Q8YK18 anabaena sp
38	19	76.0	261	16	Q930V4	Q930V4 rhizobium m
39	19	76.0	261	16	Q8ZN43	Q8ZN43 salmonella
40	19	76.0	261	16	Q8Z4N4	Q8Z4N4 salmonella
41	19	76.0	261	16	Q8X2E7	Q8X2E7 escherichia
42	19	76.0	262	11	Q9JW46	Q9JW46 rattus norv
43	19	76.0	262	17	G8TUK3	G8TUK3 methanosarc
44	19	76.0	265	10	Q8RY01	Q8RY01 arabidopsis
45	19	76.0	268	16	Q9A034	Q9A034 streptococc

ALIGNMENTS

RESULT 1

Q8V6S0 PRELIMINARY; PRT; 70 AA.
ID Q8V6S0
AC Q8V6S0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 7.6 kDa protein.
OS Halovirus HF2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=33771;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Fisher C., Nuttall S.D., Dyal-Smith M.L.;
RT "Sequence and transcription of halovirus HF2."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF222060; AAL54955.1; -
KW Hypothetical protein.
SQ SEQUENCE 70 AA; 7583 MW; 64BCED165C9C761A CRC64;

Query Match 76.0% Score 19; DB 12; Length 70;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXTLXL 8
Db 42 DLSLTL 47

RESULT 2

Q94ML6 PRELIMINARY; PRT; 76 AA.
ID Q94ML6
AC Q94ML6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Membrane protein p9.
OS Bacteriophage phi-12.
OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.

```

OX NCBI_TaxID=161736;
RP [1]
RN SEQUENCE FROM N.A.
RA Gottlieb P., Wei H., Toporovsky I.;
RT "Nucleotide Sequence of the Small dRNA Segment of Phi12.";
RL Nucleotide Sequence of the Small dRNA Segment of Phi12.;
DR EMBL: AY034425; ARK60442.1; -
SQ SEQUENCE 76 AA; 8065 MW; 9CC9BC7C31EC3DCD CRC64;

Query Match
Best Local Similarity 76.0%; Score 19; DB 9; Length 76;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 31 DSLTTL 36

RESULT 3
Q9RW66 PRELIMINARY; PRT; 80 AA.
ID Q9RW66
AC Q9RW66
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein DR0803.
GN DR0803.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001935; AAF10390.1; -
DR TIGR; DR0803; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 80 AA; 8384 MW; BB64E97CFE772891 CRC64;

Query Match
Best Local Similarity 76.0%; Score 19; DB 16; Length 80;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 43 DALTSL 48

RESULT 4
Q9TTA7 PRELIMINARY; PRT; 101 AA.
ID Q9TTA7
AC Q9TTA7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cation-independent mannose 6-phosphate receptor (fragment).
OS Macropus fuliginosus (Western gray kangaroo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9316;
RN [1]
RP SEQUENCE FROM N.A.

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RA Yandell C.A., Dunbar A.J., Wheldrake J.F., Upton Z.;
RT "The kangaroo cation-independent mannose 6-phosphate receptor binds
RT insulin-like growth factor-II.";
RL J. Biol. Chem. 0:0-0(2000).
DR EMBL: AF168361; AAF19161.1; -
KW Receptor.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 11014 MW; 9956DF42C4421EC1 CRC64;

Query Match
Best Local Similarity 76.0%; Score 19; DB 6; Length 101;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 14 DALTSL 19

RESULT 5
Q9S217 PRELIMINARY; PRT; 115 AA.
ID Q9S217
AC Q9S217
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SC01783.
GN SC01783 OR SC151.23C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Krieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Krieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL109848; CAB52847.1; -
KW Hypothetical protein.
SQ SEQUENCE 115 AA; 11960 MW; F867BB2E0D842308 CRC64;

Query Match
Best Local Similarity 66.7%; Score 19; DB 16; Length 115;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 82 DALTSL 87

RESULT 6
Q8U346 PRELIMINARY; PRT; 118 AA.
ID Q8U346
AC Q8U346
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0626.
GN PF0626.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;

```

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
RX  Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RA  "The complete sequence of the Pyrococcus furiosus genome.";
RT  Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL  EMBL: AE010184; AAL80750.1;
RW  Hypothetical protein; Complete proteome.
SQ  SEQUENCE 118 AA; 13587 MW; 58DF1662D4934ADE CRC64;

Query Match 76.0%; Score 19; DB 17; Length 118;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DLTXL 8
Db 89 DLTAL 94

RESULT 7
Q9HMY9 PRELIMINARY; PRT; 123 AA.
ID Q9HMY9
AC Q9HMY9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Vng2324h.
GN Vng2324h.
OS Halobacterium sp. (strain NRC-11).
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leitthausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassearna S.;
RT "Genome sequence of Halobacterium species NRC-11";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AE005115; AAG20432.1;
DR InterPro: IPR003675; Abi.
DR Pfam: PF02517; Abi; 1.
KW Complete proteome.
SQ SEQUENCE 123 AA; 12639 MW; 78021F5C708F44A6 CRC64;

Query Match 76.0%; Score 19; DB 17; Length 123;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DLTXL 8
Db 108 DALTL 113

RESULT 8
Q92BU2 PRELIMINARY; PRT; 125 AA.
ID Q92BU2
AC Q92BU2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein lin1452.
GN LIN1452.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CLIP 11262 / SEROVAR 6A;
RX  PubMed=11679669;
RA  Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Barche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Kuhn M., Kunz F., Kurapkut G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL: AL596168; CAC96683.1;
DR ListList; LIN01452;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 125 AA; 14508 MW; B3D62278280D0F8A CRC64;

Query Match 76.0%; Score 19; DB 16; Length 125;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DLTXL 8
Db 62 DLTTL 67

RESULT 9
Q9SA59 PRELIMINARY; PRT; 129 AA.
ID Q9SA59
AC Q9SA59;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE F1003.7.
GN F1003.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A., Altafi H.,
RA Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen M.,
RA Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F1003 sequence.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006550; AAD25798.1;
DR InterPro: IPR003612; AAI.
DR InterPro: IPR000528; Plant_LTP.
DR InterPro: IPR001768; Try/amil_inhtr.
DR Pfam: PF00234; try_alpha_ami1; 1.
DR PRINTS: PR00382; LIPIDTRANSFER.
DR SMART: SM00499; AAI; 1.
SQ SEQUENCE 129 AA; 13967 MW; 789A42465A1F931E CRC64;

Query Match 76.0%; Score 19; DB 10; Length 129;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3 DMLTXL 8
DB 27 DMLTSL 32

RESULT 10
Q47480
ID Q47480 PRELIMINARY; PRT; 146 AA.
AC Q47480;
DT 01-JUN-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF146.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90170953; PubMed=2155230;
RA Chen C.-M., Ye Q.-Z., Zhu Z., Wanner B.L., Walsh C.T.;
RT "Molecular biology of carbon-phosphorus bond cleavage: Cloning and
RT sequencing of the phn (psiD) genes involved in alkylphosphate uptake
RT and C-P lyase activity in Escherichia coli B.";
RL J. Biol. Chem. 265:4461-4471(1990).
DR EMBL; J05260; AAA24342.1; -
SQ SEQUENCE 146 AA; 16141 MW; 16BFE691EC0347C9 CRC64;

Query Match 76.0%; Score 19; DB 2; Length 146;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DMLTXL 8
DB 61 DMLTSL 66

RESULT 11
Q9CDM1 PRELIMINARY; PRT; 148 AA.
ID Q9CDM1
AC Q9CDM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown protein.
GN YHID OR L12198.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=IL1403;
RA MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AB006449; AAK06296.1; -
KW Complete proteome.
SQ SEQUENCE 148 AA; 16681 MW; 68980E6750367671 CRC64;

Query Match 76.0%; Score 19; DB 16; Length 148;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DMLTXL 8
DB 8 DMLTSL 13

RESULT 12
Q9R6Q3 PRELIMINARY; PRT; 157 AA.
ID Q9R6Q3;
AC Q9R6Q3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein TTE2738.
GN TTE2738.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013213; AA025851.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 157 AA; 17807 MW; 1BBAC96507A5C03 CRC64;

Query Match 76.0%; Score 19; DB 16; Length 157;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DMLTXL 8
DB 146 DMLTSL 151

RESULT 13
Q96K17 PRELIMINARY; PRT; 158 AA.
ID Q96K17
AC Q96K17;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ114844 fis. clone PLACE100133, highly similar to transcription
DE factor BTF3 (Hypothetical 17.3 kDa protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabeekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahata K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP SEQUENCE FROM N.A.
RX TISSUE=PROSTATIC ADENOCARCINOMA;
RA Strausberg R.;
RN Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK027750; BAB55342.1; -
DR EMBL; BC022371; AAH22371.1; -
DR InterPro; IPR002745; NAC.
DR Pfam; PF01849; NAC; 1.
KW Hypothetical protein.
SQ SEQUENCE 158 AA; 17270 MW; 8C4AD056FB92D722 CRC64;

Query Match 76.0%; Score 19; DB 4; Length 158;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Martinez-Garcia E.;
 RT "gen ipos y fenotipo gasp en enterobacterias.";
 RL Thesis (2001), Department of Bioquimica y Biologia molecular.,
 DR EMBL; AJ422108; CAD19472.1; --
 KW Hypothetical protein
 SQ SEQUENCE 165 AA; 18317 MW; 2E76215144730D4E CRC64;
 Query Match 76.0%; Score 19; DB 2; Length 165;
 Best Local Similarity 66.7%; Pred. No. 6.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DXTLXL 8
 DB 72 DLTSL 113

Search completed: May 24, 2003, 17:12:41
 Job time : 29 secs

QY 3 DXTLXL 8
 DB 108 DLTSL 113

RESULT 14
 Q9CQH7 PRELIMINARY; PRT; 158 AA.
 AC Q9CQH7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 4632412E09Rik protein (Similar to putative).
 GN 4632412E09Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukuishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Iyoy-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK013120; BAB28660.1; --
 DR EMBL; AK004239; BAB23233.1; --
 DR EMBL; AK011367; BAB27573.1; --
 DR EMBL; BC024612; AAH24612.1; --
 DR EMBL; BC024920; AAH24920.1; --
 DR WGD; MGI:1913312; 4632412E09Rik.
 DR InterPro; IPR002715; NAC.
 DR Pfam; PF01849; NAC; 1.
 SQ SEQUENCE 158 AA; 17270 MW; 8C4AD058F92D722 CRC64;
 Query Match 76.0%; Score 19; DB 11; Length 158;
 Best Local Similarity 66.7%; Pred. No. 6.5e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DXTLXL 8
 DB 108 DLTSL 113

RESULT 15
 Q9VNT5 PRELIMINARY; PRT; 165 AA.
 AC Q9VNT5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 18.3 kDa protein.

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: May 24, 2003, 17:00:41 ; Search time 31 Seconds
(without alignments)

42.984 Million cell updates/sec

Title: US-09-932-613-448

Perfect score: 25

Sequence: 1 XDXLTXLXX 10

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	76.0	32	14	AA1983148 Acetobacter diagan
2	19	76.0	49	22	ABG181384 Novel human diagno
3	19	76.0	62	22	AA1985810 Human immune/haema
4	19	76.0	69	22	AA1989883 Human immune/haema
5	19	76.0	72	22	AA1987450 Propionibacterium
6	19	76.0	77	22	AAU62909 C. symbiosum gluta
7	19	76.0	87	20	AA1980048 Human stomach canc
8	19	76.0	100	22	AA1984009 Human protein sequ
9	19	76.0	100	22	AB1982222 Novel human diagno
10	19	76.0	104	22	ABG20532

11	19	76.0	135	19	AAW76230 Bacterial periplas
12	19	76.0	145	21	AAG15400 Arabidopsis thalia
13	19	76.0	148	23	AB155553 Lactococcus lactis
14	19	76.0	151	23	ABP42341 Human ovarian anti
15	19	76.0	153	21	ABG15399 Arabidopsis thalia
16	19	76.0	157	23	ABP42459 Human ovarian anti
17	19	76.0	158	22	ABG04427 Novel human diagno
18	19	76.0	158	22	ABG09338 Novel human diagno
19	19	76.0	158	22	ABG27645 Novel human diagno
20	19	76.0	158	22	AA194026 Human stomach canc
21	19	76.0	158	22	AA198651 Human protein sequ
22	19	76.0	158	22	AB194608 Human eukaryotic
23	19	76.0	158	23	AB181213 Arabidopsis thalia
24	19	76.0	159	22	ABG17907 Arabidopsis thalia
25	19	76.0	160	21	AA15398 Human cancer assoc
26	19	76.0	173	21	AA193809 Human colon cancer
27	19	76.0	173	22	ABG73827 Sequence of DNA en
28	19	76.0	174	15	AB194582 Human ovarian anti
29	19	76.0	179	23	ABP42354 Human secreted pro
30	19	76.0	180	20	AA192543 Human transcriptio
31	19	76.0	185	22	AB123116 Human protein SEQ
32	19	76.0	185	22	AA196335 Human secreted pro
33	19	76.0	188	21	AA196166 Novel signal trans
34	19	76.0	193	22	AA197195 Novel signal trans
35	19	76.0	199	22	AA197572 Streptococcus poly
36	19	76.0	205	23	AB192973 Streptococcus poly
37	19	76.0	211	23	AB192977 Propionibacterium
38	19	76.0	213	22	AA1963590 Novel human diagno
39	19	76.0	220	22	ABG21553 Human EST encoded
40	19	76.0	224	22	AA194300 Propionibacterium
41	19	76.0	241	22	AA190029 Novel human diagno
42	19	76.0	242	22	ABG29725 Novel human diagno
43	19	76.0	252	22	ABG04428 Streptococcus poly
44	19	76.0	253	23	AB190356 Escherichia coli p
45	19	76.0	261	22	AA198451

ALIGNMENTS

RESULT 1

AA1983148

ID AA1983148 standard; peptide; 32 AA.

XX AA1983148;

XX AA1983148;

DT 13-OCT-1993 (first entry)

XX Acetobacter diguanylate cyclase partial sequence.

DE Cyclic diguanylate; diguanylate phosphodiesterase;

KW diguanylate cyclase; cellulose production.

XX Acetobacter xylinum.

OS Acetobacter xylinum.

XX Key Location/Qualifiers

FT Misc-difference 29..31

PT /note= "three amino acid residues not identified"

XX WO9311244-A.

XX 10-JUN-1993.

XX 14-OCT-1992; 92WO-US08756.

XX 29-NOV-1991; 91US-0800218.

XX (WEYE) WEYERHAEUSER CO.

XX Ben-Bassat A, Ben-Ziman M, Calhoon RD, Gelfand DH;

XX Tal R, Wong HC;

XX WPI; 1993-197062/24.

XX Polynucleotide sequence from Acetobacter cdg operon - encodes
PT cyclic di:guanosine mono:phosphate degradation enzymes e.g.
PT 3-phosphodiesterase isozyme
XX
PS Example 2; Page 30; 98pp; English.
XX
CC Four polypeptide bands were isolated from Acetobacter using a GMP
CC affinity column. The first two bands (I and II) had diguanylate
CC phosphodiesterase activity and the second two (III and IV) had
CC diguanylate cyclase activity. The band III peptide was oxidised
CC with performic acid and the partial digest was dialysed, then
CC digested with lysyl endopeptidase from Achromobacter. The resulting
CC peptides were separated by HPLC and sequenced. The sequence of
CC fraction 50 (AAR38148) was used as the basis for designing
CC oligonucleotide pools for cloning the diguanylate cyclase gene.
XX
SQ Sequence 32 AA;
Query Match 76.0%; Score 19; DB 14; Length 32;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DXLTXL 8
| | | |
DB 8 DLTTL 13
| | | |
RESULT 2
ABG18384
ID ABG18384 standard; Protein; 49 AA.
XX
AC ABG18384;
XX
DT 18-FEB-2002 (first entry)
DE
DE Novel human diagnostic protein #18375.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US08531.
XX
XX 31-MAR-2000; 2000US-0540217.
PR
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSB-) HYSBQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR
XX N-PSDB; AAS82571.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
XX Claim 20; SEQ ID No 48743; 103pp; English.
PS
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 49 AA;
Query Match 76.0%; Score 19; DB 22; Length 49;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DXLTXL 8
| | | |
DB 11 DALTTL 16
| | | |
RESULT 3
AAM85810
ID AAM85810 standard; Protein; 62 AA.
XX
AC AAM85810;
XX
DT 07-NOV-2001 (first entry)
DE
DE Human immune/haematopoietic antigen SEQ ID NO:13403.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
XX Homo sapiens.
OS
XX WO200157182-A2.
PN
XX 09-AUG-2001.
PD
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR
XX 04-FEB-2000; 2000US-0180628.
PR
XX 24-FEB-2000; 2000US-0184664.
PR
XX 02-MAR-2000; 2000US-0186350.
PR
XX 16-MAR-2000; 2000US-0189874.
PR
XX 17-MAR-2000; 2000US-0190076.
PR
XX 18-APR-2000; 2000US-0198123.
PR
XX 19-MAY-2000; 2000US-0205515.
PR
XX 07-JUN-2000; 2000US-0209467.
PR
XX 28-JUN-2000; 2000US-0214896.
PR
XX 30-JUN-2000; 2000US-0215135.
PR
XX 07-JUL-2000; 2000US-0216647.
PR
XX 07-JUL-2000; 2000US-0216980.
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XX 11-JUL-2000; 2000US-0217487.
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XX 14-JUL-2000; 2000US-0217496.
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XX 26-JUL-2000; 2000US-0218290.
PR
XX 26-JUL-2000; 2000US-0220963.
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XX 26-JUL-2000; 2000US-0220964.
PR
XX 14-AUG-2000; 2000US-0224518.
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XX 14-AUG-2000; 2000US-0224519.
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XX 14-AUG-2000; 2000US-0225213.
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XX 14-AUG-2000; 2000US-0225266.
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XX 14-AUG-2000; 2000US-0225267.
PR
XX 14-AUG-2000; 2000US-0225268.
PR
XX 14-AUG-2000; 2000US-0225269.
PR
XX 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0235758.
PR 18-AUG-2000; 2000US-0236279.
PR 22-AUG-2000; 2000US-0236279.
PR 22-AUG-2000; 2000US-0236681.
PR 22-AUG-2000; 2000US-0236868.
PR 22-AUG-2000; 2000US-0237182.
PR 23-AUG-2000; 2000US-0237009.
PR 30-AUG-2000; 2000US-0228934.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231958.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.

PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX N-PSDB; AAK58591.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Claim 11; SEQ ID NO 13403; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I/
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins, and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.

XX Sequence 62 AA;
SQ
Query Match 76.0%; Score 19; DB 22; Length 62;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;

Matches	4;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	3	DXLTXL 8							
Db	2	DSLTL 7							
RESULT 4									
AAM89883									
ID	AAM89883 standard; Protein; 69 AA.								
XX	AAM89883;								
XX	07-NOV-2001 (first entry)								
XX	Human immune/haematopoietic antigen SEQ ID NO:17476.								
XX	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;								
XX	cytostatic; Gene therapy; vaccine; metastasis.								
XX	Homo sapiens.								
XX	WO200157182-A2.								
XX	08-AUG-2001.								
XX	17-JAN-2001; 2001WO-US01354.								
XX	31-JAN-2000; 2000US-0179065.								
XX	04-FEB-2000; 2000US-0180228.								
XX	24-FEB-2000; 2000US-0184664.								
XX	02-MAR-2000; 2000US-0186350.								
XX	16-MAR-2000; 2000US-0189874.								
XX	17-MAR-2000; 2000US-0190076.								
XX	18-APR-2000; 2000US-0198123.								
XX	19-MAY-2000; 2000US-0205515.								
XX	07-JUN-2000; 2000US-0209467.								
XX	28-JUN-2000; 2000US-0214886.								
XX	30-JUN-2000; 2000US-0215135.								
XX	07-JUL-2000; 2000US-0216647.								
XX	11-JUL-2000; 2000US-0217487.								
XX	11-JUL-2000; 2000US-0217496.								
XX	14-JUL-2000; 2000US-0218290.								
XX	26-JUL-2000; 2000US-0220363.								
XX	26-JUL-2000; 2000US-0220964.								
XX	14-AUG-2000; 2000US-0224518.								
XX	14-AUG-2000; 2000US-0224519.								
XX	14-AUG-2000; 2000US-0225213.								
XX	14-AUG-2000; 2000US-0225214.								
XX	14-AUG-2000; 2000US-0225266.								
XX	14-AUG-2000; 2000US-0225267.								
XX	14-AUG-2000; 2000US-0225268.								
XX	14-AUG-2000; 2000US-0225270.								
XX	14-AUG-2000; 2000US-0225447.								
XX	14-AUG-2000; 2000US-0225757.								
XX	14-AUG-2000; 2000US-0225758.								
XX	14-AUG-2000; 2000US-0225759.								
XX	18-AUG-2000; 2000US-0226279.								
XX	22-AUG-2000; 2000US-0226681.								
XX	22-AUG-2000; 2000US-0226868.								
XX	22-AUG-2000; 2000US-0227182.								
XX	23-AUG-2000; 2000US-0227009.								
XX	30-AUG-2000; 2000US-0228924.								
XX	01-SEP-2000; 2000US-0229287.								
XX	01-SEP-2000; 2000US-0229343.								
XX	01-SEP-2000; 2000US-0229344.								
XX	01-SEP-2000; 2000US-0229345.								
XX	05-SEP-2000; 2000US-0229509.								
XX	05-SEP-2000; 2000US-0229513.								
XX	06-SEP-2000; 2000US-0230437.								
XX	06-SEP-2000; 2000US-0230438.								
XX	08-SEP-2000; 2000US-0231242.								
XX	08-SEP-2000; 2000US-0231243.								
XX	08-SEP-2000; 2000US-0231244.								
XX	08-SEP-2000; 2000US-0231413.								
XX	08-SEP-2000; 2000US-0231414.								
XX	08-SEP-2000; 2000US-0232080.								
XX	08-SEP-2000; 2000US-0232081.								
XX	12-SEP-2000; 2000US-0231968.								
XX	14-SEP-2000; 2000US-0232397.								
XX	14-SEP-2000; 2000US-0232398.								
XX	14-SEP-2000; 2000US-0232399.								
XX	14-SEP-2000; 2000US-0232400.								
XX	14-SEP-2000; 2000US-0232401.								
XX	14-SEP-2000; 2000US-0233063.								
XX	14-SEP-2000; 2000US-0233064.								
XX	14-SEP-2000; 2000US-0233065.								
XX	21-SEP-2000; 2000US-0234223.								
XX	21-SEP-2000; 2000US-0234274.								
XX	25-SEP-2000; 2000US-0234997.								
XX	25-SEP-2000; 2000US-0234998.								
XX	26-SEP-2000; 2000US-0235484.								
XX	27-SEP-2000; 2000US-0235834.								
XX	27-SEP-2000; 2000US-0235836.								
XX	29-SEP-2000; 2000US-0236327.								
XX	29-SEP-2000; 2000US-0236367.								
XX	29-SEP-2000; 2000US-0236368.								
XX	29-SEP-2000; 2000US-0236369.								
XX	02-OCT-2000; 2000US-0236370.								
XX	02-OCT-2000; 2000US-0236802.								
XX	02-OCT-2000; 2000US-0237037.								
XX	02-OCT-2000; 2000US-0237038.								
XX	02-OCT-2000; 2000US-0237039.								
XX	02-OCT-2000; 2000US-0237040.								
XX	13-OCT-2000; 2000US-0239935.								
XX	13-OCT-2000; 2000US-0239937.								
XX	20-OCT-2000; 2000US-0240960.								
XX	20-OCT-2000; 2000US-0241221.								
XX	20-OCT-2000; 2000US-0241785.								
XX	20-OCT-2000; 2000US-0241786.								
XX	20-OCT-2000; 2000US-0241787.								
XX	20-OCT-2000; 2000US-0241808.								
XX	20-OCT-2000; 2000US-0241826.								
XX	01-NOV-2000; 2000US-0244617.								
XX	08-NOV-2000; 2000US-0246474.								
XX	08-NOV-2000; 2000US-0246475.								
XX	08-NOV-2000; 2000US-0246476.								
XX	08-NOV-2000; 2000US-0246477.								
XX	08-NOV-2000; 2000US-0246478.								
XX	08-NOV-2000; 2000US-0246523.								
XX	08-NOV-2000; 2000US-0246524.								
XX	08-NOV-2000; 2000US-0246525.								
XX	08-NOV-2000; 2000US-0246526.								
XX	08-NOV-2000; 2000US-0246527.								
XX	08-NOV-2000; 2000US-0246528.								
XX	08-NOV-2000; 2000US-0246532.								
XX	08-NOV-2000; 2000US-0246609.								
XX	08-NOV-2000; 2000US-0246610.								
XX	08-NOV-2000; 2000US-0246611.								
XX	08-NOV-2000; 2000US-0246613.								
XX	17-NOV-2000; 2000US-0249207.								
XX	17-NOV-2000; 2000US-0249208.								
XX	17-NOV-2000; 2000US-0249209.								
XX	17-NOV-2000; 2000US-0249210.								
XX	17-NOV-2000; 2000US-0249211.								
XX	17-NOV-2000; 2000US-0249212.								
XX	17-NOV-2000; 2000US-0249213.								
XX	17-NOV-2000; 2000US-0249214.								
XX	17-NOV-2000; 2000US-0249215.								
XX	17-NOV-2000; 2000US-0249216.								
XX	17-NOV-2000; 2000US-0249217.								
XX	17-NOV-2000; 2000US-0249218.								
XX	17-NOV-2000; 2000US-0249244.								
XX	17-NOV-2000; 2000US-0249245.								

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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0253678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
DR N-PSDB; AAK62664.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Claim 11; SEQ ID NO 17476; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 69 AA;
SQ
Query Match 76.0%; Score 19; DB 22; Length 69;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 DXLTXL 8
Db 9 DSLTAL 14
RESULT 5
AAK87450
ID AAK87450 standard; Protein; 72 AA.
XX
AC AAK87450;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:15043.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.

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XX OS Homo sapiens.
XX FN WO200157182-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01354.
XX
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 11-JUL-2000; 2000US-0217496.
XX PR 14-JUL-2000; 2000US-0218290.
XX PR 26-JUL-2000; 2000US-0220963.
XX PR 26-JUL-2000; 2000US-0220964.
XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0224519.
XX PR 14-AUG-2000; 2000US-0225213.
XX PR 14-AUG-2000; 2000US-0225214.
XX PR 14-AUG-2000; 2000US-0225266.
XX PR 14-AUG-2000; 2000US-0225267.
XX PR 14-AUG-2000; 2000US-0225268.
XX PR 14-AUG-2000; 2000US-0225270.
XX PR 14-AUG-2000; 2000US-0225447.
XX PR 14-AUG-2000; 2000US-0225757.
XX PR 14-AUG-2000; 2000US-0225758.
XX PR 18-AUG-2000; 2000US-0226279.
XX PR 22-AUG-2000; 2000US-0226681.
XX PR 22-AUG-2000; 2000US-0226688.
XX PR 22-AUG-2000; 2000US-0227182.
XX PR 23-AUG-2000; 2000US-0227009.
XX PR 30-AUG-2000; 2000US-0228924.
XX PR 01-SEP-2000; 2000US-0229287.
XX PR 01-SEP-2000; 2000US-0229343.
XX PR 01-SEP-2000; 2000US-0229344.
XX PR 01-SEP-2000; 2000US-0229345.
XX PR 05-SEP-2000; 2000US-0229509.
XX PR 05-SEP-2000; 2000US-0229513.
XX PR 06-SEP-2000; 2000US-0230437.
XX PR 06-SEP-2000; 2000US-0230438.
XX PR 08-SEP-2000; 2000US-0231242.
XX PR 08-SEP-2000; 2000US-0231243.
XX PR 08-SEP-2000; 2000US-0231244.
XX PR 08-SEP-2000; 2000US-0231413.
XX PR 08-SEP-2000; 2000US-0231414.
XX PR 08-SEP-2000; 2000US-0232080.
XX PR 08-SEP-2000; 2000US-0232081.
XX PR 12-SEP-2000; 2000US-0231968.
XX PR 14-SEP-2000; 2000US-0232397.
XX PR 14-SEP-2000; 2000US-0232398.
XX PR 14-SEP-2000; 2000US-0232399.
XX PR 14-SEP-2000; 2000US-0232400.
XX PR 14-SEP-2000; 2000US-0232401.
XX PR 14-SEP-2000; 2000US-0233063.
XX PR 14-SEP-2000; 2000US-0233064.
XX PR 14-SEP-2000; 2000US-0233065.
XX PR 21-SEP-2000; 2000US-0234223.
XX PR 21-SEP-2000; 2000US-0234274.
XX PR 25-SEP-2000; 2000US-0234997.
XX PR 25-SEP-2000; 2000US-0234998.
XX PR 25-SEP-2000; 2000US-0234999.

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PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX XX
 DR WPI, 2001-483426/52.
 XX DR N-PSDB; AAK60231.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX XX
 PS Claim 11; SEQ ID NO 15043; 3071pp + Sequence Listing; English.
 XX XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
 CC represent sequences used in the exemplification of the present invention.
 XX XX
 SQ Sequence 72 AA;
 Query Match 76.0%; Score 19; DB 22; Length 72;
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 DLTSL 8
 DB 24 DLTSL 23
 RESULT 6
 ID AAK62909
 XX AAK62909 standard; Protein; 77 AA.
 AC AAK62909;
 XX DT 27-FEB-2002 (first entry)
 XX DE Propionibacterium acnes immunogenic protein #23805.
 XX KW SAPRO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX OS Propionibacterium acnes.
 XX PN WO200181581-A2.
 XX PD 01-NOV-2001.
 XX PF 20-APR-2001; 2001WO-US12865.
 XX PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX XX
 PA (CORI-) CORIXA CORP.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59630.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 XX Example 1; SEQ ID NO 24104; 1069pp; English.
 PS
 SS Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 77 AA;

Query Match 76.0%; Score 19; DB 22; Length 77;
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 DLTXL 8
 Db 41 DLTSL 46

RESULT 7
 AAW90048
 ID AAW90048 standard; Protein; 87 AA.
 XX
 AC AAW90048;
 XX
 DF 26-FEB-1999 (first entry)
 XX
 DE C. symbiosum glutamate dehydrogenase fragment #2.
 XX
 KW Phenylalanine dehydrogenase; pdh; L-amino acid; phenylpyruvic acid;
 KW aspartame production; phenylketonuria; infant; glutamate dehydrogenase;
 KW diet.
 OS
 SS Clostridium symbiosum.
 XX
 PN US5851810-A.
 XX
 PD 22-DEC-1998.
 XX
 PF 05-JUN-1995; 95US-0461990.
 XX
 PR 05-JUN-1995; 95US-0461990.
 XX
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 XX
 PI Blanchard JS;
 XX
 DR WPI; 1999-080406/07.
 XX
 PT DNA encoding Rhodococcus L-phenylalanine dehydrogenase - for

PT production of recombinant enzyme
 XX
 PS Disclosure; Fig 5; 30pp; English.
 XX

CC This sequence is used to describe a method which results in the isolation
 CC of a phenylalanine dehydrogenase protein, pdh, from Rhodococcus sp. M4.
 CC The encoding pdh nucleic acid is used to produce recombinant Rhodococcus
 CC L-phenylalanine dehydrogenase, which can be used to produce L-amino acids
 CC from the corresponding alpha-keto acids, e.g. to produce L-phenylalanine
 CC from phenylpyruvic acid (e.g. for the production of aspartame), to screen
 CC for phenylketonuria in newborn infants and to monitor the efficacy of
 CC low-phenylalanine diets.

SQ Sequence 87 AA;

Query Match 76.0%; Score 19; DB 20; Length 87;
 Best Local Similarity 66.7%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 DLTXL 8
 Db 36 DLTSL 41

RESULT 8
 AAM94009
 ID AAM94009 standard; Protein; 100 AA.
 XX
 AC AAM94009;
 XX

DT 13-NOV-2001 (first entry)

DE Human stomach cancer expressed polypeptide SEQ ID NO 88.
 XX
 KW Human; stomach cancer; marker; screening; micro-metastasis;
 KW peritoneal dissemination.

OS Homo sapiens.

PN WO200109317-A1.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-JP05063.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 18-OCT-1999; 99US-0159590.

PR 11-JAN-2000; 2000JP-0118776.

PR 17-FEB-2000; 2000US-0183322.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;

PI Kodama T, Midorikawa Y;

DR WPI; 2001-570287/64.

DR N-PSDB; AAI93886.

XX

PT New Stomach cancer-associated genes, useful as markers in blood tests
 PT for screening for the early stages of the disease -

PS Claim 1; Page 162-163; 242pp; Japanese.

XX

CC The invention relates to stomach cancer-expressed genes
 CC (AAI93842-AAI93917) and the encoded proteins (AAM93967-AAM94039). The
 CC genes can be used as markers in blood tests for screening for the early
 CC stages of the disease. The proteins and peptides can be used as targets
 CC for screening for compounds to treat the disease. They can also be used
 CC for predicting micro-metastases. The gene can predict peritoneal

CC dissemination.
XX
SQ Sequence 100 AA;

Query Match 76.0%; Score 19; DB 22; Length 100;
Best Local Similarity 66.7%; Pred. NO. 4.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXTLXL B
| | | |
Db 50 DSLTSL 55

RESULT 9

ID AAB95222 standard; Protein; 100 AA.

XX
AC AAB95222;

XX
DT 26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:17346.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX
KW Homo sapiens.

XX
OS EP1074617-A2.

XX
PN 07-FEB-2001.

XX
PD 28-JUL-2000; 2000EP-0116126.

XX
PF 29-JUL-1999; 99JP-0248036.

XX
PR 27-AUG-1999; 99JP-030253.

XX
PR 11-JAN-2000; 2000JP-0118776.

XX
PR 02-MAY-2000; 2000JP-0183767.

XX
PR 09-JUN-2000; 2000JP-0241899.

XX
PA (HELI-) HELIX RES INST.

XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX
PI WPI; 2001-318749/34.

XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
full-length cDNAs defined in the specification, and for the detection
and/or diagnosis of the abnormality of the proteins encoded by the
full-length cDNAs -

XX
PS Claim 8; SEQ ID 17346; 2537pp + CD ROM; English.

XX
CC The present invention describes primer sets for synthesizing 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence/3'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesizing polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification
of the present invention.

SQ Sequence 100 AA;

Query Match 76.0%; Score 19; DB 22; Length 100;
Best Local Similarity 66.7%; Pred. NO. 4.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXTLXL B
| | | |
Db 50 DSLTSL 55

RESULT 10

ID ABG20532 standard; Protein; 104 AA.

XX
AC ABG20532;

XX
DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #20523.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.

XX
OS Homo sapiens.

XX
PN WO200175067-A2.

XX
PD 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000; 2000US-0540217.

XX
PR 23-AUG-2000; 2000US-0649167.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Drmanac RT, Liu C, Tang YT;

XX
PI WPI; 2001-639362/73.

XX
DR N-PSDB; AAS84719.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity -

XX
PS Claim 20; SEQ ID No 50891; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymerase chain reaction (PCR) primers, oligomers, and for chromosome
and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
to restore normal activity of (II) or to treat disease states involving
(II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
imaging of sites expressing (II). (I) and (II) are useful for treating
disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. ABG00010-ABG30377 represent novel human
diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pt_sequences.

XX SQ Sequence 104 AA;
Query Match 76.0%; Score 19; DB 22; Length 104;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXTLXL 8
DB 53 DSLTAL 58

RESULT 11
AAW76230
ID AAW76230 standard; protein; 135 AA.
XX AC
XX AC AAW76230;
XX DT
XX DT 02-DEC-1998 (first entry)
XX DE
XX DE Bacterial periplasmic binding protein fragment #5.
XX KW
XX KW Protein-ligand binding pocket; PLBP; binding protein; ligand; modulator;
XX KW bacterial periplasmic binding protein; interaction energies; ischaemia;
XX KW basis set molecules; BSM; ionotropic glutamate receptors; treatment;
XX KW neuroprotectant; stroke; epilepsy; neuropathic pain;
XX OS
XX OS Prokaryota.
XX PN
XX PN W09838208-A2.
XX PD
XX PD 03-SEP-1998.
XX PF
XX PF 27-FEB-1998; 98WO-US03951.
XX PR
XX PR 28-FEB-1997; 97US-0808004.
XX PA
XX PA (BEAR-) BEARDSDEN BIO INC.
XX PI
XX PI Sturgess M;
XX DR
XX DR WPI; 1998-495386/42.
XX PT
XX PT Designing a model for a ligand-binding pocket in a protein and its
XX PT use for assessing ligand affinity - without the need to prepare test
XX PT ligand, for identifying selective antagonists for ionotropic
XX PT glutamate receptors, potentially useful as neuroprotectants with
XX PT reduced side effects
XX PS
XX PS Disclosure; Page 211; 218pp; English.
XX CC
XX CC AAW76226-W76250 are protein fragments used in the design of a model of a
XX CC protein-ligand binding pocket (PLBP) of a binding protein. A model is
XX CC constructed based on topographic similarity to the binding pocket of a
XX CC bacterial periplasmic binding protein. The model is refined by energy
XX CC minimisation, with a high affinity ligand in the binding pocket.
XX CC Interaction energies of basis set molecules (BSM) are obtained by
XX CC calculating energy of the models for the binding pocket BP and BSM
XX CC individually (Er and Em) and total energy (Exm) of bound complexes
XX CC formed. The model is used to predict the selectivity of a potential
XX CC ligand for a set of related PLBP's, specifically ionotropic glutamate
XX CC receptors. Identified ligands are potentially useful for studying
XX CC receptor binding and activity and as modulators of receptor activity
XX CC (or lead compounds for developing such compounds). The ligands are
XX CC potentially useful therapeutically, e.g. as neuroprotectants during
XX CC ischaemia and for treatment of stroke, head injuries, epilepsy,
XX CC neuropathic pain etc. The method allows affinity of ligands to be
XX CC estimated without having to prepare them and then test them, in vitro.
XX CC Ligands with high selectivity for particular glutamate receptors
XX CC should have fewer side effects than known receptor antagonists.

XX SQ Sequence 135 AA;

Query Match 76.0%; Score 19; DB 19; Length 135;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DXTLXL 8
DB 48 DALTSL 53

RESULT 12
AAG15400
ID AAG15400 standard; Protein; 145 AA.
XX AC
XX AC AAG15400;
XX DT
XX DT 17-OCT-2000 (first entry)
XX DE
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 15638.
XX KW
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS
XX OS Arabidopsis thaliana.
XX PN
XX PN EP1033405-A2.
XX PD
XX PD 06-SEP-2000.
XX PF
XX PF 25-FEB-2000; 2000BP-0301439.
XX PR
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 03-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0128845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 28-APR-1999; 99US-0130891.
XX PR 28-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.
XX PR 30-APR-1999; 99US-0132407.
XX PR 04-MAY-1999; 99US-0132484.
XX PR 05-MAY-1999; 99US-0132485.
XX PR 06-MAY-1999; 99US-0132486.
XX PR 07-MAY-1999; 99US-0132487.
XX PR 11-MAY-1999; 99US-0132863.
XX PR 14-MAY-1999; 99US-0134256.
XX PR 14-MAY-1999; 99US-0134218.
XX PR 14-MAY-1999; 99US-0134219.
XX PR 14-MAY-1999; 99US-0134221.
XX PR 14-MAY-1999; 99US-0134370.
XX PR 18-MAY-1999; 99US-0134768.
XX PR 19-MAY-1999; 99US-0134941.
XX PR 20-MAY-1999; 99US-0135124.
XX PR 21-MAY-1999; 99US-0135353.
XX PR 24-MAY-1999; 99US-0135629.
XX PR 25-MAY-1999; 99US-0136021.
XX PR 27-MAY-1999; 99US-0136392.
XX PR 28-MAY-1999; 99US-0136782.
XX PR 01-JUN-1999; 99US-0137222.
XX PR 03-JUN-1999; 99US-0137528.
XX PR 04-JUN-1999; 99US-0137502.
XX PR 07-JUN-1999; 99US-0137724.
XX PR 08-JUN-1999; 99US-0138094.
XX PR 10-JUN-1999; 99US-0138540.
XX PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.
PR 15-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 19-JUN-1999; 99US-0139456.
PR 20-JUN-1999; 99US-0139457.
PR 21-JUN-1999; 99US-0139458.
PR 22-JUN-1999; 99US-0139459.
PR 23-JUN-1999; 99US-0139460.
PR 24-JUN-1999; 99US-0139461.
PR 25-JUN-1999; 99US-0139462.
PR 26-JUN-1999; 99US-0139463.
PR 27-JUN-1999; 99US-0139464.
PR 28-JUN-1999; 99US-0139465.
PR 29-JUN-1999; 99US-0139466.
PR 30-JUN-1999; 99US-0139467.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 03-JUL-1999; 99US-0142255.
PR 04-JUL-1999; 99US-0142390.
PR 05-JUL-1999; 99US-0142803.
PR 06-JUL-1999; 99US-0142920.
PR 07-JUL-1999; 99US-0142977.
PR 08-JUL-1999; 99US-0143342.
PR 09-JUL-1999; 99US-0143362.
PR 10-JUL-1999; 99US-0144005.
PR 11-JUL-1999; 99US-0144085.
PR 12-JUL-1999; 99US-0144086.
PR 13-JUL-1999; 99US-0144325.
PR 14-JUL-1999; 99US-0144331.
PR 15-JUL-1999; 99US-0144332.
PR 16-JUL-1999; 99US-0144333.
PR 17-JUL-1999; 99US-0144334.
PR 18-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144336.
PR 20-JUL-1999; 99US-0144337.
PR 21-JUL-1999; 99US-0144338.
PR 22-JUL-1999; 99US-0144339.
PR 23-JUL-1999; 99US-0144340.
PR 24-JUL-1999; 99US-0144341.
PR 25-JUL-1999; 99US-0144342.
PR 26-JUL-1999; 99US-0144343.
PR 27-JUL-1999; 99US-0144344.
PR 28-JUL-1999; 99US-0144345.
PR 29-JUL-1999; 99US-0144346.
PR 30-JUL-1999; 99US-0144347.
PR 01-AUG-1999; 99US-0144348.
PR 02-AUG-1999; 99US-0144349.
PR 03-AUG-1999; 99US-0144350.
PR 04-AUG-1999; 99US-0144351.
PR 05-AUG-1999; 99US-0144352.
PR 06-AUG-1999; 99US-0144353.
PR 07-AUG-1999; 99US-0144354.
PR 08-AUG-1999; 99US-0144355.
PR 09-AUG-1999; 99US-0144356.
PR 10-AUG-1999; 99US-0144357.
PR 11-AUG-1999; 99US-0144358.
PR 12-AUG-1999; 99US-0144359.
PR 13-AUG-1999; 99US-0144360.
PR 14-AUG-1999; 99US-0144361.
PR 15-AUG-1999; 99US-0144362.
PR 16-AUG-1999; 99US-0144363.
PR 17-AUG-1999; 99US-0144364.
PR 18-AUG-1999; 99US-0144365.
PR 19-AUG-1999; 99US-0144366.
PR 20-AUG-1999; 99US-0144367.
PR 21-AUG-1999; 99US-0144368.
PR 22-AUG-1999; 99US-0144369.
PR 23-AUG-1999; 99US-0144370.
PR 24-AUG-1999; 99US-0144371.
PR 25-AUG-1999; 99US-0144372.
PR 26-AUG-1999; 99US-0144373.
PR 27-AUG-1999; 99US-0144374.
PR 28-AUG-1999; 99US-0144375.
PR 29-AUG-1999; 99US-0144376.
PR 30-AUG-1999; 99US-0144377.

PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
PR 14-AUG-1999; 99US-0148384.
PR 15-AUG-1999; 99US-0148385.
PR 16-AUG-1999; 99US-0148386.
PR 17-AUG-1999; 99US-0148387.
PR 18-AUG-1999; 99US-0148388.
PR 19-AUG-1999; 99US-0148389.
PR 20-AUG-1999; 99US-0148390.
PR 21-AUG-1999; 99US-0148391.
PR 22-AUG-1999; 99US-0148392.
PR 23-AUG-1999; 99US-0148393.
PR 24-AUG-1999; 99US-0148394.
PR 25-AUG-1999; 99US-0148395.
PR 26-AUG-1999; 99US-0148396.
PR 27-AUG-1999; 99US-0148397.
PR 28-AUG-1999; 99US-0148398.
PR 29-AUG-1999; 99US-0148399.
PR 30-AUG-1999; 99US-0148400.
PR 01-SEP-1999; 99US-0151303.
PR 02-SEP-1999; 99US-0151304.
PR 03-SEP-1999; 99US-0151305.
PR 04-SEP-1999; 99US-0151306.
PR 05-SEP-1999; 99US-0151307.
PR 06-SEP-1999; 99US-0151308.
PR 07-SEP-1999; 99US-0151309.
PR 08-SEP-1999; 99US-0151310.
PR 09-SEP-1999; 99US-0151311.
PR 10-SEP-1999; 99US-0151312.
PR 11-SEP-1999; 99US-0151313.
PR 12-SEP-1999; 99US-0151314.
PR 13-SEP-1999; 99US-0151315.
PR 14-SEP-1999; 99US-0151316.
PR 15-SEP-1999; 99US-0151317.
PR 16-SEP-1999; 99US-0151318.
PR 17-SEP-1999; 99US-0151319.
PR 18-SEP-1999; 99US-0151320.
PR 19-SEP-1999; 99US-0151321.
PR 20-SEP-1999; 99US-0151322.
PR 21-SEP-1999; 99US-0151323.
PR 22-SEP-1999; 99US-0151324.
PR 23-SEP-1999; 99US-0151325.
PR 24-SEP-1999; 99US-0151326.
PR 25-SEP-1999; 99US-0151327.
PR 26-SEP-1999; 99US-0151328.
PR 27-SEP-1999; 99US-0151329.
PR 28-SEP-1999; 99US-0151330.
PR 29-SEP-1999; 99US-0151331.
PR 30-SEP-1999; 99US-0151332.
PR 01-OCT-1999; 99US-0151333.
PR 02-OCT-1999; 99US-0151334.
PR 03-OCT-1999; 99US-0151335.
PR 04-OCT-1999; 99US-0151336.
PR 05-OCT-1999; 99US-0151337.
PR 06-OCT-1999; 99US-0151338.
PR 07-OCT-1999; 99US-0151339.
PR 08-OCT-1999; 99US-0151340.
PR 09-OCT-1999; 99US-0151341.
PR 10-OCT-1999; 99US-0151342.
PR 11-OCT-1999; 99US-0151343.
PR 12-OCT-1999; 99US-0151344.
PR 13-OCT-1999; 99US-0151345.
PR 14-OCT-1999; 99US-0151346.
PR 15-OCT-1999; 99US-0151347.
PR 16-OCT-1999; 99US-0151348.
PR 17-OCT-1999; 99US-0151349.
PR 18-OCT-1999; 99US-0151350.
PR 19-OCT-1999; 99US-0151351.
PR 20-OCT-1999; 99US-0151352.
PR 21-OCT-1999; 99US-0151353.
PR 22-OCT-1999; 99US-0151354.
PR 23-OCT-1999; 99US-0151355.
PR 24-OCT-1999; 99US-0151356.
PR 25-OCT-1999; 99US-0151357.
PR 26-OCT-1999; 99US-0151358.
PR 27-OCT-1999; 99US-0151359.
PR 28-OCT-1999; 99US-0151360.
PR 29-OCT-1999; 99US-0151361.
PR 30-OCT-1999; 99US-0151362.

Query Match 76.0%; Score 19; DB 21; Length 145;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTXTL 8
DB 98 DLTAL 103

RESULT 13

ABBS5553
ID ABB5553 standard; Protein; 148 AA.

XX AC ABB55553;
XX 16-MAY-2002 (first entry)
XX Lactococcus lactis protein ywID.
XX Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX OS Lactococcus lactis IL1403.
XX FR2807446-A1.
XX 12-OCT-2001.
XX 11-APR-2000; 2000FR-0004630.
XX 11-APR-2000; 2000FR-0004630.
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX WPI; 2002-043418/06.
XX New nucleotide sequence useful in the identification of Lactococcus
XX lactis and related species -
XX Claim 6; SEQ ID NO 2255; 2504pp; French.
XX The present invention is related to a Lactococcus lactis nucleotide
XX sequence (ABA90521) and related proteins (ABBS53300-ABBS5621). The
XX nucleic acid sequence is useful in the detection and/or amplification of
XX related species. The proteins of the invention are useful for the
XX biosynthesis or biodegradation of a composition of interest. The
XX invention helps research in lactic bacteria, particularly useful in the
XX production of yogurt and cheese.
XX Note: The sequence data for this patent is based on equivalent patent
XX WO200177334 (published 18-OCT-2001) which is available in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 148 AA;

Query Match 76.0%; Score 19; DB 23; Length 148;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 8 DSLTAL 13

RESULT 14

ABP42341
ID ABP42341 standard; Protein; 151 AA.

XX AC ABP42341;
XX 22-AUG-2002 (first entry)
XX Human ovarian antigen HNOQA93, SEQ ID NO:3473.
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW Gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX OS Homo sapiens.
XX WO200200677-A1.
XX 03-JAN-2002.
XX 07-JUN-2001; 2001WO-US18569.
XX 07-JUN-2000; 2000US-209467P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
XX WPI; 2002-147878/19.
XX N-PSDB; ABQ55418.
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases -
XX Claim 11; SEQ ID No 3473; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP42228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 93% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides which
XX modulate ovarian antigen expression or activity. The polynucleotides may
XX further be used for gene therapy, chromosome mapping, in the
XX identification of individuals and in forensic analysis, and the
XX polypeptides may be used as food additives or to prepare antibodies
XX useful in disease diagnosis, drug targeting and phenotyping. The present
XX sequence represents a human ovarian antigen of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 151 AA;

Query Match 76.0%; Score 19; DB 23; Length 151;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXLTXL 8
Db 102 DSLTSL 107

RESULT 15
AAG15399

PR 23-AUG-1999; 99US-0149910.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154772.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 76.0%; Score 19; DB 21; Length 153;
Best Local Similarity 66.7%; Pred. No. 6.6e-02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DXTXL 8
Db 106 DALTAL 111

Search completed: May 24, 2003, 17:11:21
Job time : 33 secs

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FILE 'REGISTRY' ENTERED AT 18:49:39 ON 24 MAY 2003
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 23 MAY 2003 HIGHEST RN 519387-75-8
DICTIONARY FILE UPDATES: 23 MAY 2003 HIGHEST RN 519387-75-8

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 6, 2003

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

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DEL HIS

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L2 1 S L1 AND 10/SQL
L3 26541 S ..D.LT.L../SQSP
L4 3 S L3 AND 10/SQL
L5 2 S L4 NOT L2

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L6 0 S L2 OR L5

FILE 'USPATFULL, USPAT2' ENTERED AT 18:49:09 ON 24 MAY 2003

L7 0 S L2 OR L5

FILE 'HCAPLUS' ENTERED AT 18:49:14 ON 24 MAY 2003

L8 2 S L2 OR L5

FILE 'REGISTRY' ENTERED AT 18:49:39 ON 24 MAY 2003

=> d sqide can l2

L2 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS

RN 402495-85-6 REGISTRY

CN L-Leucine, L-tryptophyl-L-tyrosyl-L-.alpha.-aspartyl-L-prolyl-L-leucyl-L-
threonyl-L-lysyl-L-leucyl-L-tryptophyl- (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 278: PN: WO0216412 SEQID: 436 claimed sequence

CN 370: PN: WO0216411 SEQID: 436 claimed sequence

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 10

PATENT ANNOTATIONS (PNTE):

Sequence | Patent

Source | Reference

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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Not Given|WO2002016411
         |claimed
         |SEQID 436
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         |WO2002016412
         |claimed
         |SEQID 436

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SEQ 1 WYDPLTKLWL

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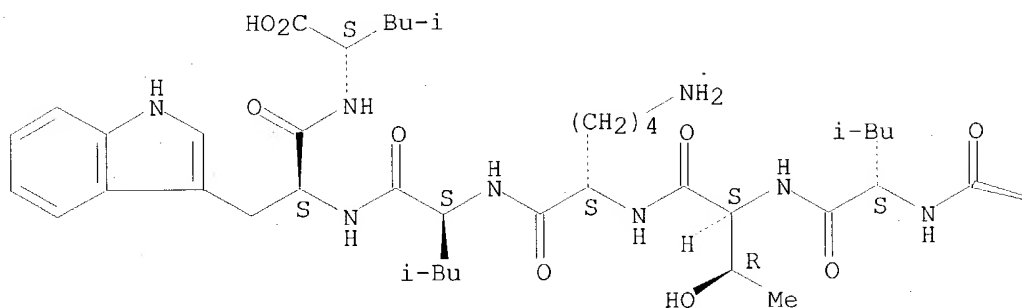
MF C68 H95 N13 O15

SR CA

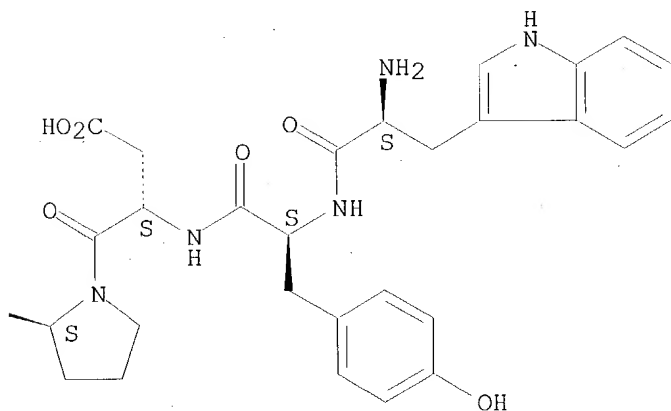
LC STN Files: CA, CAPLUS, TOXCENTER

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



2 REFERENCES IN FILE CA (1957 TO DATE)
2 REFERENCES IN FILE CAPLUS (1957 TO DATE)

REFERENCE 1: 136:215418

REFERENCE 2: 136:215417

=> d sqide can 15 tot

L5 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2003 ACS
 RN 402545-90-8 REGISTRY
 CN Peptide, (Xaa-Xaa-Asp-Xaa-Leu-Thr-Xaa-Leu-Xaa-Xaa) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 47: PN: WO0216412 SEQID: 448 claimed protein
 FS PROTEIN SEQUENCE
 SQL 10
 NTE

type	location	description
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uncommon	Aaa-2	-
uncommon	Aaa-4	-
uncommon	Aaa-7	-
uncommon	Aaa-9	-
uncommon	Aaa-10	-

PATENT ANNOTATIONS (PNTE):

Sequence |Patent
 Source |Reference

=====
 Not Given|WO2002016412
 |claimed
 |SEQID 448

SEQ 1 XXDXLTXLXX

HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

1 REFERENCES IN FILE CA (1957 TO DATE)

1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

REFERENCE 1: 136:215418

L5 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2003 ACS
 RN 402545-43-1 REGISTRY
 CN Peptide, (Xaa-Xaa-Asp-Xaa-Leu-Thr-Xaa-Leu-Xaa-Xaa) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 382: PN: WO0216411 SEQID: 448 claimed protein
 FS PROTEIN SEQUENCE
 SQL 10
 NTE

type	location	description
uncommon	Aaa-1	-
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uncommon	Aaa-4	-
uncommon	Aaa-7	-
uncommon	Aaa-9	-

uncommon Aaa-10 - -

PATENT ANNOTATIONS (PNTE):

Sequence |Patent
Source |Reference

=====+=====

Not Given|WO2002016411

|claimed
|SEQID 448

SEQ 1 XXDXLTXLXX

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HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

1 REFERENCES IN FILE CA (1957 TO DATE)

1 REFERENCES IN FILE CAPLUS (1957 TO DATE)

REFERENCE 1: 136:215417

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 18:49:53 ON 24 MAY 2003

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FILE COVERS 1907 - 24 May 2003 VOL 138 ISS 22

FILE LAST UPDATED: 23 May 2003 (20030523/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d all tot 18

L8 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:157817 HCAPLUS

DN 136:215418

TI B lymphocyte stimulator protein-binding polypeptides for BLyS detection and purification

IN Beltzer, James P.; Potter, M. Daniel; Fleming, Tony J.; Ladner, Robert Charles

PA Dyax Corp., USA

SO PCT Int. Appl., 269 pp.

CODEN: PIXXD2

DT Patent
 LA English
 IC ICM C07K007-00
 CC 15-5 (Immunochemistry)
 Section cross-reference(s): 3, 9

FAN.CNT 1

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PI	WO 2002016412	A2	20020228	WO 2001-US25891	20010817
	W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
	RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
	AU 2001085066	A5	20020304	AU 2001-85066	20010817
PRAI	US 2000-226489P	P	20000818		
	WO 2001-US25891	W	20010817		
OS	MARPAT 136:215418				
AB	Binding polypeptides comprising specific amino acid sequences are disclosed that bind B Lymphocyte Stimulator (BLyS) protein or BlyS-like polypeptides. The binding polypeptides can be used in methods of the invention for detecting or isolating BlyS protein or BlyS-like polypeptides in solns. or mixts., such as blood, tissue samples, or conditioned media.				
ST	B lymphocyte stimulator protein binding polypeptide; BLyS binding peptide purifn				
IT	Animal Bacteriophage Chromatographic stationary phases Chromatography Culture media Mixtures Phage display library Solutions (B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)				
IT	DNA RL: BSU (Biological study, unclassified); BIOL (Biological study) (B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)				
IT	Cytokines RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); ANST (Analytical study); BIOL (Biological study); PREP (Preparation) (BAFF; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)				
IT	Human Monkey Mouse Rat (BLyS from; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)				
IT	Peptides, biological studies Proteins RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses) (BLyS-binding; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)				

IT Proteins
 RL: ANT (Analyte); BSU (Biological study, unclassified); PUR (Purification or recovery); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
 (BLYS-like; B lymphocyte stimulator protein (BLYS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Cytokine receptors
 RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
 (BLYS; B lymphocyte stimulator protein (BLYS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Proteins
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (sepn.; B lymphocyte stimulator protein (BLYS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT

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RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

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RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT	402549-95-5P, Cytokine BAFF (rat fragment)	402549-96-6P, Cytokine BAFF (rat isoform fragment)
	402549-97-7P, Cytokine BAFF (rat isoform fragment)	402549-98-8P, Cytokine BAFF (rat isoform fragment)
	402549-99-9P, Cytokine BAFF (monkey fragment)	402550-00-9P, Cytokine BAFF (monkey isoform fragment)
	402550-01-0P, Cytokine BAFF (human)	402550-02-1P, Cytokine BAFF (human isoform)
	402550-03-2P, Cytokine BAFF (mouse)	402550-04-3P, Cytokine BAFF (mouse isoform)

RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(amino acid sequence; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT	402550-27-0
	RL: PRP (Properties)
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IT	402550-25-8 402550-26-9 402550-28-1

RL: PRP (Properties)
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 polypeptides for BLyS detection and purifn.)
 IT 98849-88-8 402491-95-6 402493-28-1
 RL: PRP (Properties)
 (unclaimed sequence; b lymphocyte stimulator protein-binding
 polypeptides for BLyS detection and purifn.)

L8 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2003 ACS
 AN 2002:157816 HCAPLUS
 DN 136:215417
 TI B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis
 and treatment of immunological disorders
 IN Beltzer, James P.; Potter, Daniel M.; Fleming, Tony L.; Rosen, Craig A.
 PA Human Genome Sciences, Inc., USA
 SO PCT Int. Appl., 387 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC ICM C07K007-00
 CC 15-5 (Immunochemistry)
 Section cross-reference(s): 3
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002016411	A2	20020228	WO 2001-US25850	20010817
	W:		AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
	RW:		GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG		
	AU 2001088301	A5	20020304	AU 2001-88301	20010817
	US 2003091565	A1	20030515	US 2001-932613	20010817
PRAI	US 2000-226700P	P	20000818		
	WO 2001-US25850	W	20010817		
AB	Binding polypeptides that specifically bind BLyS protein or BLyS-like polypeptides can be used in methods of the invention for detecting, diagnosing, or prognosing a disease or disorder assocd. with aberrant BLyS or BLyS receptor expression or inappropriate function of BLyS or BLyS receptor, comprising BLyS binding polypeptides or fragments or variants thereof, that specifically bind to BLyS. The present invention further relates to methods and compns. for preventing, treating or ameliorating a disease or disorder assocd. with aberrant BLyS or BLyS receptor expression or inappropriate BLyS function or BLyS receptor function, comprising administering to an animal, preferably a human, an effective amt. of one or more BLyS binding polypeptides or fragments or variants thereof, that specifically bind to BLyS. The aberrant BLyS or BLyS receptor expression conditions include immunol. diseases, autoimmune diseases, immunodeficiency, lupus, glomerular nephritis, rheumatoid arthritis, multiple sclerosis, hypogammaglobulinemia or hypergammaglobulinemia, graft vs. host disease, cancer, infectious disease, leukemia, lymphoma, hematopoietic cell proliferative disease, chronic lymphocytic leukemia, multiple myeloma, non-Hodgkin's lymphoma, Hodgkin's disease, T cell proliferative disease, acute myelogenous leukemia, etc.				
ST	BLyS receptor binding peptide autoimmune disease; cancer immunol disease				
	BLyS binding peptide				
IT	Immunoglobulins				
	RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP				

- (Preparation); USES (Uses)
(A; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Cell activation
Cell proliferation
(B cell; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Animal
Antitumor agents
Autoimmune disease
DNA sequences
Hodgkin's disease
Human
Immunodeficiency
Infection
Leukemia
Lupus erythematosus
Lymphoma
Molecular cloning
Multiple myeloma
Multiple sclerosis
Phage display library
Prognosis
Protein sequences
Rheumatoid arthritis
Transplant rejection
(B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Immunoglobulins
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Leukemia
Lymphoma
(B-cell; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Cytokines
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(BAFF; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Cytokine receptors
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(BLyS; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Immunoglobulins
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(G; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Immunoglobulins
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(M; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)
- IT Cell proliferation
(T cell; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT B cell (lymphocyte)
(activation; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Leukemia
(acute myelogenous; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Neoplasm
(benign; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Diagnosis
(cancer; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Leukemia
(chronic lymphocytic; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Neoplasm
(diagnosis; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT B cell (lymphocyte)
Lymphocyte
Macrophage
Monocyte
T cell (lymphocyte)
(disease, proliferative; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Immunity
(disorder; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Hematopoiesis
(disorders, proliferative; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Kidney, disease
(glomerulonephritis; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Transplant and Transplantation
(graft-vs.-host reaction; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Immunoglobulins
(hypogammaglobulinemia; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Lymphoma
(non-Hodgkin's; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT B cell (lymphocyte)
T cell (lymphocyte)
(proliferation; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Dendritic cell
(proliferative disease; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Disease, animal
(proliferative; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT Globulins, biological studies
RL: ADV (Adverse effect, including toxicity); BSU (Biological study, unclassified); BIOL (Biological study)
(.gamma.-, hypergammaglobulinemia; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT 402491-96-7 402491-97-8 402491-98-9 402491-99-0 402492-00-6
402492-01-7 402492-02-8 402492-03-9 402492-04-0 402492-05-1
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RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT	402494-44-4	402494-45-5	402494-46-6	402494-47-7	402494-48-8
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 402545-40-8 402545-41-9 402545-42-0 **402545-43-1**

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT 402549-77-3P, Cytokine BAFF (human 285-amino acid) 402549-78-4P, Cytokine BAFF (human 266-amino acid) 402549-79-5P, Cytokine BAFF (mouse 309-amino acid) 402549-80-8P, Cytokine BAFF (mouse 290-amino acid) 402549-81-9P 402549-82-0P 402549-83-1P 402549-84-2P 402549-85-3P, Cytokine BAFF (monkey 243-amino acid) 402549-86-4P

RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (amino acid sequence; B lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT 402550-22-5 402550-24-7

RL: PRP (Properties)
 (unclaimed nucleotide sequence; b lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT 402550-23-6

RL: PRP (Properties)
 (unclaimed protein sequence; b lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

IT 98849-88-8 402491-95-6 402493-28-1 402550-20-3 402550-21-4

RL: PRP (Properties)
 (unclaimed sequence; b lymphocyte stimulator protein (BLyS) binding polypeptides for diagnosis and treatment of immunol. disorders)

=> d his

(FILE 'HOME' ENTERED AT 18:45:09 ON 24 MAY 2003)

DEL HIS

FILE 'REGISTRY' ENTERED AT 18:46:27 ON 24 MAY 2003

L1 263 S [WEKCLARGS][YFECN]D[PSTFLYCA]LT[KNQGR]L[WSTRCYK][LFVIH]/SQSP
 SAV L1 ROARK932613/A
 L2 1 S L1 AND 10/SQL
 L3 26541 S ..D.LT.L../SQSP
 L4 3 S L3 AND 10/SQL
 L5 2 S L4 NOT L2

L6 FILE 'HCAOLD' ENTERED AT 18:49:05 ON 24 MAY 2003
0 S L2 OR L5

L7 FILE 'USPATFULL, USPAT2' ENTERED AT 18:49:09 ON 24 MAY 2003
0 S L2 OR L5

L8 FILE 'HCAPLUS' ENTERED AT 18:49:14 ON 24 MAY 2003
2 S L2 OR L5

FILE 'REGISTRY' ENTERED AT 18:49:39 ON 24 MAY 2003

FILE 'HCAPLUS' ENTERED AT 18:49:53 ON 24 MAY 2003
SEL RN L8

FILE 'REGISTRY' ENTERED AT 18:50:30 ON 24 MAY 2003

L9 491 S E1-E491
L10 488 S L9 NOT L2,L4,L5
L11 248 S L10 AND L1
L12 281 S L10 AND L3
L13 281 S L11,L12

DESCRIPTORS:

Mammal... Poultry...

colony stimulating factor of human manuf. by immunodeficient

Animal tissue culture...

colony stimulating factor of human manuf. by, of lymphoblastoids

Lymphoblast...

human colony stimulating factor manuf. by

Immunodeficiency...

human colony stimulating factor manuf. in nonhuman animal in

Animal cell line,BALL-1... Animal cell line,JBL... Animal cell line,NALL-1

... Animal cell line,Namalwa... Animal cell line,TALL-1...

Hybridoma...

Kidney,carcinoma,neoplasm... Lung,carcinoma,neoplasm...

Lymphocyte,B-...

Salivary gland,submandibular, neoplasm...

Stomach,carcinoma,neoplasm...

human colony stimulating factor manuf. with

CAS REGISTRY NUMBERS:

62683-29-8P manuf. of human, by lymphoblastoid cell culture

10/7/297 (Item 24 from file: 399)

DIALOG(R)File 399:CA SEARCH(R)

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105030965 CA: 105(4)30965x JOURNAL

Determination of the Kirkwood-Buff integral from experimental data

AUTHOR(S): Zaitseva, A. L.; Kessler, Yu. M.; Kiselev, M. G.; Gerasimov, A. V.

LOCATION: Inst. Khim. Nevodn. Rastvorov, Ivanovo, USSR

JOURNAL: Zh. Fiz. Khim. DATE: 1986 VOLUME: 60

NUMBER: 5 PAGES: 1280-3

CODEN: ZFKHA9 ISSN: 0044-4537 LANGUAGE: Russian SECTION:

CA169002 Thermodynamics, Thermochemistry, and Thermal Properties

CA168XXX Phase Equilibriums, Chemical Equilibriums, and Solutions

IDENTIFIERS: free energy compn binary system relation

DESCRIPTORS:

Liquid structure...

of binary soln., partial free energies of components in relation to

Chemical potential...

of component of binary systems, soln. compn. in relation to ? ds

Set Items Description

S1 1397 (BLYS OR BAFF OR ZTNF4 OR THANK OR TALL(W)1 OR TALL(W)I)/TI

S2 740 RD S1 (unique items)

S3 2528 (BLYS OR BAFF OR ZTNF4 OR THANK OR TALL(W)1 OR TALL(W)I)/AB

S4 1504 RD S3 (unique items)

S5 2056 S2 OR S4

S6 2028 RD S5 (unique items)

S7 1417 S6 AND PY<2002

S8 1550 (BLYS OR BAFF OR ZTNF4 OR TALL(W)1 OR TALL(W)I)/AB OR (BLYS

OR BAFF OR ZTNF4 OR TALL(W)1 OR

TALL(W)I)/TI

S9 611 RD S8 (unique items)

S10 297 S9 AND PY<2002

? logoff y

07jul04 15:45:49 User226352 Session D781.3

\$20.65 3.688 DialUnits File5

\$241.50 138 Type(s) in Format 7

\$241.50 138 Types

\$262.15 Estimated cost File5

\$2.52 0.427 DialUnits File6

\$5.70 3 Type(s) in Format 7

\$5.70 3 Types

\$8.22 Estimated cost File6

\$54.96 2.681 DialUnits File34

\$220.15 37 Type(s) in Format 7

\$220.15 37 Types

\$275.11 Estimated cost File34

\$0.47 0.068 DialUnits File40

\$1.30 1 Type(s) in Format 7

\$1.30 1 Types

\$1.77 Estimated cost File40

\$3.35 0.745 DialUnits File50

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\$94.00 47 Types

\$97.35 Estimated cost File50

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\$6.60 6 Type(s) in Format 7

\$6.60 6 Types

\$9.11 Estimated cost File65

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\$12.32 7 Types

\$20.04 Estimated cost File71

\$20.29 2.071 DialUnits File73

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\$35.10 13 Types

\$55.39 Estimated cost File73

\$2.19 0.627 DialUnits File94

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\$5.40 4 Types

\$7.59 Estimated cost File94

\$0.68 0.285 DialUnits File98

\$11.55 7 Type(s) in Format 5

\$3.35 1 Type(s) in Format 7

\$14.90 8 Types

\$15.58 Estimated cost File98

\$4.24 0.832 DialUnits File103

\$4.95 3 Type(s) in Format 7

\$4.95 3 Types

\$9.19 Estimated cost File103

\$0.33 0.138 DialUnits File143

\$0.33 Estimated cost File143

\$7.40 2.114 DialUnits File144

\$16.50 10 Type(s) in Format 7

\$16.50 10 Types

\$23.90 Estimated cost File144

\$9.22 2.880 DialUnits File155

\$1.05 5 Type(s) in Format 7

\$1.05 5 Types

\$10.27 Estimated cost File155

\$2.83 0.529 DialUnits File156

\$0.95 1 Type(s) in Format 7

\$0.95 1 Types

\$3.78 Estimated cost File156

\$0.86 0.191 DialUnits File162

\$2.00 1 Type(s) in Format 7

\$2.00 1 Types

\$2.86 Estimated cost File162

\$0.48 0.049 DialUnits File172

\$0.48 Estimated cost File172

\$1.08 0.139 DialUnits File305

\$1.08 Estimated cost File305

\$0.27 0.076 DialUnits File369

\$0.27 Estimated cost File369

? ds

Set	Items	Description
S1	11000	TALL(W)1 OR BAFF OR BLYS OR THANK OR ZTNF4 OR NEUTROKINE
S2	2251	S1 AND (MONOCLONAL OR ANTIBOD? OR MAB OR AB)
S3	2018	RD S2 (unique items)
S4	1720	S3 AND PY<2002
S5	1430	S4 AND (ANTAGON? OR INHIBIT? OR REDUC? OR NEUTRALIZ?)
S6	1044	S5 AND (THERAP? OR TREAT? OR ADMINIS?)
S7	478	S6 AND IN(W)VIVO
S8	9	S7/DE
S9	396	S5 (10N) (THERAP? OR TREAT? OR ADMINIS?)

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